







01-MAY-1998 (TREMUR) 10, Created  
 01-MAY-1998 (TREMUR) 10, Last sequence update  
 01-OCT-2000 (TREMUR) 15, Last annotation update  
 MELATONIN RECEPTOR MELA (FRAGMENT)  
 Mesocricetus auratus (Golden hamster)  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Cricetidae:  
 Mesocricetus  
 NCBI\_Taxid=10036;  
 (1)  
 SEQUENCE FROM N.A.  
 TISSUE=SUPRACHIASMATIC NUCLEI;  
 Author: F. Schuster, C. Polirel, V. J. Pevet, P. Masson-Pevet M.;  
 "Cloning experiments and developmental expression of both melatonin  
 receptor mRNA and melatonin binding sites in the Syrian hamster  
 suprachiasmatic nuclei".  
 Brain Res Mol Brain Res 0:0-0(1998)  
 DR EMBL: AF061158 AAC67241.1;  
 DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR000276;  
 DR PFAM: PF00001; 7tm\_1; 1;  
 DR PRINTS: PR00237; 3P3RHDQSN;  
 DR PRINTS: PR00857; MELATONIN;  
 DR PRINTS: PR01012; NEPEPTIDE;  
 DR PRINTS: PR01149; MELATONINAR;  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEPTOR, UNKNOWN\_1  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 325  
 FT SEQUENCE 325 AA 46781 MW: A98406C07EDABAS CRC64;

Query Match 58.3% Score 1074; 25.11; Length 305;  
 Best Local Similarity 62.6% Pred No. 13878;  
 Matches 199 Conservative 61 Mismatches 62 Gaps 1

01-MAY-1998 (TREMUR) 10, Created  
 01-MAY-1998 (TREMUR) 10, Last sequence update  
 01-OCT-2000 (TREMUR) 15, Last annotation update  
 MELATONIN RECEPTOR MELA (FRAGMENT)  
 Mesocricetus auratus (Golden hamster)  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Cricetidae:  
 Mesocricetus  
 NCBI\_Taxid=10036;  
 (1)  
 SEQUENCE FROM N.A.  
 TISSUE=SUPRACHIASMATIC NUCLEI;  
 Author: F. Schuster, C. Polirel, V. J. Pevet, P. Masson-Pevet M.;  
 "Cloning experiments and developmental expression of both melatonin  
 receptor mRNA and melatonin binding sites in the Syrian hamster  
 suprachiasmatic nuclei".  
 Brain Res Mol Brain Res 0:0-0(1998)  
 DR EMBL: AF061158 AAC67241.1;  
 DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR000276;  
 DR PFAM: PF00001; 7tm\_1; 1;  
 DR PRINTS: PR00237; 3P3RHDQSN;  
 DR PRINTS: PR00857; MELATONIN;  
 DR PRINTS: PR01012; NEPEPTIDE;  
 DR PRINTS: PR01149; MELATONINAR;  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEPTOR, UNKNOWN\_1  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 325  
 FT SEQUENCE 325 AA 46781 MW: A98406C07EDABAS CRC64;

Mammalia: Eutheria: Sciurognathi: Muridae: Cricetidae:  
 Mesocricetus  
 NCBI\_Taxid=10036;  
 (1)  
 SEQUENCE FROM N.A.  
 TISSUE=SUPRACHIASMATIC NUCLEI;  
 Author: F. Schuster, C. Polirel, V. J. Pevet, P. Masson-Pevet M.;  
 "Cloning experiments and developmental expression of both melatonin  
 receptor mRNA and melatonin binding sites in the Syrian hamster  
 suprachiasmatic nuclei".  
 Brain Res Mol Brain Res 0:0-0(1998)  
 DR EMBL: AF061158 AAC67241.1;  
 DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR000276;  
 DR PFAM: PF00001; 7tm\_1; 1;  
 DR PRINTS: PR00237; 3P3RHDQSN;  
 DR PRINTS: PR00857; MELATONIN;  
 DR PRINTS: PR01012; NEPEPTIDE;  
 DR PRINTS: PR01149; MELATONINAR;  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEPTOR, UNKNOWN\_1  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 325  
 FT SEQUENCE 325 AA 46781 MW: A98406C07EDABAS CRC64;

Query Match 58.0% Score 1049; 25.11; Length 305;  
 Best Local Similarity 62.6% Pred No. 13878;  
 Matches 199 Conservative 61 Mismatches 62 Gaps 1

01-MAY-1998 (TREMUR) 10, Created  
 01-MAY-1998 (TREMUR) 10, Last sequence update  
 01-OCT-2000 (TREMUR) 15, Last annotation update  
 MELATONIN RECEPTOR MELA (FRAGMENT)  
 Mesocricetus auratus (Golden hamster)  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Cricetidae:  
 Mesocricetus  
 NCBI\_Taxid=10036;  
 (1)  
 SEQUENCE FROM N.A.  
 TISSUE=SUPRACHIASMATIC NUCLEI;  
 Author: F. Schuster, C. Polirel, V. J. Pevet, P. Masson-Pevet M.;  
 "Cloning experiments and developmental expression of both melatonin  
 receptor mRNA and melatonin binding sites in the Syrian hamster  
 suprachiasmatic nuclei".  
 Brain Res Mol Brain Res 0:0-0(1998)  
 DR EMBL: AF061158 AAC67241.1;  
 DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR000276;  
 DR PFAM: PF00001; 7tm\_1; 1;  
 DR PRINTS: PR00237; 3P3RHDQSN;  
 DR PRINTS: PR00857; MELATONIN;  
 DR PRINTS: PR01012; NEPEPTIDE;  
 DR PRINTS: PR01149; MELATONINAR;  
 DR PROSITE: PS00237; G\_PROTEIN\_RECEPTOR, UNKNOWN\_1  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 325  
 FT SEQUENCE 325 AA 46781 MW: A98406C07EDABAS CRC64;

DB FMRL: AF141863; AAF66601.1;  
 KW Receptor.  
 FT NONTER 174 174  
 PT NONTER 174 174  
 SO SEQUENCE 174 AA: 19857 MW: 21DDC0437E93BE77 CRC64:

Query Match 40.9% Score 780; DB 11; Length 174;  
 Best Local Similarity 84.5% Pred. No. 2.6e-55;  
 Matches 147; Conservative 9; Mismatches 18; Indels 0; Gaps 0;

149 YVYCHSMAYHRYRPMWHTPLHICLMLTVALLENFVSGLEPPRYCTFTCTACT 198  
 1 YVYCHSATYHRCQSMHAPLYISTLMLTVALLENFVSGLEPPRYCTFTCTACT 60  
 149 YVYCHSMAYHRYRPMWHTPLHICLMLTVALLENFVSGLEPPRYCTFTCTACT 258  
 149 YVYCHSMAYHRYRPMWHTPLHICLMLTVALLENFVSGLEPPRYCTFTCTACT 120  
 259 FAICWAPLNCIGLAVAINPQEMAPQIFEGCTVSYLLAFNSCLNAVYGLN 312  
 121 FAVICWAPLNCIGLAVAINPQEMAPQIFEGCTVSYLLAFNSCLNAVYGLN 174

RESULT 7

ID Q9PT13 PRELIMINARY: PRT: 162 AA.

AC Q9PT13

DT 01-MAY-2000 (TREMURel. 13, Created)

DT 01-MAY-2000 (TREMURel. 13, Last sequence update)

DT 01-OCT-2000 (TREMURel. 15, Last annotation update)

DE MELATONIN RECEPTOR (FRAGMENT).

OS Oncorhynchus mykiss (rainbow trout) (Salmo gairdneri)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Plectrocnemidae; Salmoniformes; Salmonidae; Oncorhynchus.

NC NCB1\_TaxID=8022;

KN SEQUENCE FROM N.A.

RX MEDLINE-99306591; PubMed-10379923;

RA Marzais D., Priorley I., Anglade I., Drew J., Randall C., Bromage N.,

Michael D., Kah O., Williams L.M.;

Central melatonin receptors in the rainbow trout: comparative

RT distribution of ligand binding and gene expression.

KL J. Comp. Neurol. 409:313-324(1999).

DR EMBL: AF178929; AAF66601.1;

DR INTERPRO: IPR000276;

DR INTERPRO: IPR002278;

DR PFAM: PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GCPHODOPSN.

DR PRINTS: PR00857; MELATONINR.

DR PRINTS: PR01149; MELATONINAR.

KW Receptor.

FT NONTER 162 162

FT NONTER 162 162

SO SEQUENCE 162 AA: 18895 MW: 1E1BC9151HCBA7R CRC64:

Query Match 31.0% Score 591; DB 13; Length 162;

Best Local Similarity 63.6% Pred. No. 3.4e-40;

Matches 104; Conservative 42; Mismatches 27; Indels 0; Gaps 0;

140 CYCHNSMAYHRYRPMWHTPLHICLMLTVALLENFVSGLEPPRYCTFTCTACT 159

1 CYCHNSMAYHRYRPMWHTPLHICLMLTVALLENFVSGLEPPRYCTFTCTACT 60

200 YTAWVAVHFLPLAVVSCYLPFWIVLQAPKAPKAPESPLCKPSPDLSFTLMFVAVY 259

1 YTAWVAVHFLPLAVVSCYLPFWIVLQAPKAPKAPESPLCKPSPDLSFTLMFVAVY 120

61 YTTVVAVHFLPLAVVSCYLPFWIVLQAPKAPKAPESPLCKPSPDLSFTLMFVAVY 120

260 FAICWAPLNCIGLAVAINPQEMAPQIFEGCTVSYLLAFNSCLNAVY 301

DB 121 FAVICWAPLNCIGLAVAINPQEMAPQIFEGCTVSYLLAFNSCLNAVY 162

RESULT 8

ID Q9PT17 PRELIMINARY: PRT: 161 AA

AC Q9PT17

DT 01-MAY-2000 (TREMURel. 13, Created)

DT 01-MAY-2000 (TREMURel. 13, Last sequence update)

DT 01-OCT-2000 (TREMURel. 15, Last annotation update)

DE MELATONIN RECEPTOR (FRAGMENT).

OS Oncorhynchus mykiss (rainbow trout) (Salmo gairdneri)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Plectrocnemidae; Salmoniformes; Salmonidae; Oncorhynchus.

NC NCB1\_TaxID=8022;

KN SEQUENCE FROM N.A.

RX MEDLINE-99306591; PubMed-10379923;

RA Marzais D., Priorley I., Anglade I., Drew J., Randall C., Bromage N.,

Michael D., Kah O., Williams L.M.;

Central melatonin receptors in the rainbow trout: comparative

RT distribution of ligand binding and gene expression.

KL J. Comp. Neurol. 409:313-324(1999).

DR EMBL: AF178929; AAF66601.1;

DR INTERPRO: IPR000276;

DR INTERPRO: IPR002278;

DR PFAM: PF00001; 7tm\_1; 1.

DR PRINTS: PR00237; GCPHODOPSN.

DR PRINTS: PR00857; MELATONINR.

KW Receptor.

FT NONTER 161 161

FT NONTER 161 161

SO SEQUENCE 161 AA: 18860 MW: 13BA33786512EAA3 CRC64:

Query Match 29.2% Score 556.5; DB 13; Length 161;

Best Local Similarity 59.3% Pred. No. 2e-37;

Matches 96; Conservative 34; Mismatches 31; Indels 1; Gaps 1;

140 CYCHNSMAYHRYRPMWHTPLHICLMLTVALLENFVSGLEPPRYCTFTCTACT 159

1 CYCHNSMAYHRYRPMWHTPLHICLMLTVALLENFVSGLEPPRYCTFTCTACT 60

200 YTAWVAVHFLPLAVVSCYLPFWIVLQAPKAPKAPESPLCKPSPDLSFTLMFVAVY 259

1 YTAWVAVHFLPLAVVSCYLPFWIVLQAPKAPKAPESPLCKPSPDLSFTLMFVAVY 120

61 YTTVVAVHFLPLAVVSCYLPFWIVLQAPKAPKAPESPLCKPSPDLSFTLMFVAVY 120

260 FAICWAPLNCIGLAVAINPQEMAPQIFEGCTVSYLLAFNSCLNAVY 301

121 FAVICWAPLNCIGLAVAINPQEMAPQIFEGCTVSYLLAFNSCLNAVY 161

RESULT 9

ID P70329 PRELIMINARY: PRT: 121 AA.

AC P70329

DT 01-FEB-1997 (TREMURel. 02, Created)

DT 01-FEB-1997 (TREMURel. 02, Last sequence update)

DT 01-OCT-2000 (TREMURel. 15, Last annotation update)

DE MEL-1R MELATONIN RECEPTOR (FRAGMENT).

OS Mus musculus (Mouse)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NC NCB1\_TaxID=10090;

KN SEQUENCE FROM N.A.

RA STRAIN=C57/BL6;

FA Weaver D.F., Lin G., Reppert S.M.;

Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL: U57554; AAB17865.1;

DR INTERPRO: IPR000025;

DR INTERPRO: IPR000276;

PFAM: PF00001: 7tm\_1: 1.  
 DR PRINTS: PR000857: MELATONINR.  
 FT NON\_TER 121 121  
 SEQUENCE 121 AA: 1400 MW: 42760.562906610 C6064:

Query Match 27.6% Score 527: DR 11: Length 121:  
 Best Local Similarity 80.2% Pred. No. 3.5e-35:  
 Matches 97: Conservative 11: Mismatches 13: Indels 0: Gaps 0:

QY 139 YCYCHSMAYHPIRYMHPHLCILMLTVALLPNPFVSLSEYPPYSLFICIAST 138  
 1 YCYCHSMAYHPIRYMHPHLCILMLTVALLPNPFVSLSEYPPYSLFICIAST 60  
 DB 199 QYTAAYVHIFLLPIVAVSCYPIRWIVVQAPPAKPPESLGLKPSDLPSFTMFVAV 258  
 61 QYTAAYVHIFLLPIVAVSCYPIRWIVVQAPPAKPPESLGLKPSDLPSFTMFVAV 120  
 QY 259 I 259  
 DB 121 V 121

RESULT 10  
 097777 PRELIMINARY: PRT: 138 AA

ID 097777  
 DI 01-MAY-1999 (TREMblrel. 10, Created)  
 DI 01-MAY-1999 (TREMblrel. 10, Last sequence update)  
 DI 01-JUN-2000 (TREMblrel. 14, Last annotation update)  
 DE MELATONIN RECEPTOR 1A (FRAGMENT).  
 OS Elephas maximus (Indian elephant).  
 OC Mammalia: Metazoa: Chordata: Cranialia: Vertebrata: Euteleostomi:  
 NC Mammalia: Eutheria: Proboscidea: Elephantidae: Elephas.  
 NCRI\_TaxID=4743:  
 RN [1]  
 RP SEQUENCE FROM N A  
 RA Elavsky N.E., Ernst C.W., Messer L.A., Rothschild M.F.:  
 RT Identification of Sequence Tagged Sites in the Asian Elephant  
 RL (Elephas maximus) and the African Elephant (Loxodonta africana).  
 DR EMBL: U95047: AAD00768.1:  
 DR ENTREPRO: IPR000025:  
 DR ENTREPRO: IPR000276:  
 DR ENTREPRO: IPR002278:  
 DR PFAM: PF00001: 7tm\_1: 1.  
 DR PRINTS: PR00237: GPCPHROPSN.  
 DR PRINTS: PR00857: MELATONINR.  
 DR PRINTS: PR01145: MELATONINIAK.  
 KW receptor.  
 FT NON\_TER 138 138  
 SEQUENCE 138 AA: 16116 MW: 40740.565440000 C6064:

Query Match 22.7% Score 433: DR 6: Length 138:  
 Best Local Similarity 55.5% Pred. No. 1.4e-27:  
 Matches 76: Conservative 29: Mismatches 32: Indels 0: Gaps 0:

QY 148 YHRIRPMWPHHICIMILVALLPFFVVSLEHFFYSCTFICIASTYTAAYV 207  
 2 YHRIRPMWPHHICIMILVALLPFFVVSLEHFFYSCTFICIASTYTAAYV 61  
 DB 200 HFLPLAVSCYPIRWIVVQAPPAKPPESLGLKPSDLPSFTMFVAV 257  
 62 HFLPLAVSCYPIRWIVVQAPPAKPPESLGLKPSDLPSFTMFVAV 121  
 QY 268 NCIGLAVAINPQEMAPQ 284  
 DB 122 NFIQVSLDPAKVP 138

RESULT 11  
 057463 PRELIMINARY: PRT: 375 AA.

ID 057463  
 DI 01-JUN-1998 (TREMblrel. 06, Created)  
 DI 01-JUN-1998 (TREMblrel. 06, Last sequence update)  
 DI 01-JUN-2000 (TREMblrel. 14, Last annotation update)  
 DE NEUROPEPTIDE Y /PEPTIDE Y RECEPTOR YB.  
 GN NPYRB.  
 OS Brachydontia: retio (zebrafish) (zebra danio).  
 OC Eukaryota: Metazoa: Chordata: Cranialia: Vertebrata: Euteleostomi:  
 NC Actinopterygii: Neopterygii: Teleostei: Euteleostei: Ostariophysi:  
 NC Cypriniformes: Cyprinidae: Rasbora: Danio.  
 NCRI\_TaxID=7955:  
 RN [1]  
 RP SEQUENCE FROM N A  
 RA Lundell I., Berglund M.M., Starback P., Salanck S., Gehlert D.R.,  
 RA Larhammar D.:  
 RL DNA Cell Biol. 0:0-0(1997).  
 DR EMBL: AF030245: AAB94616.1:  
 DR ZFIN: ZDB-GENE-980526-208: npyrb.  
 DR ENTREPRO: IPR000276:  
 DR ENTREPRO: IPR000611:  
 DR PFAM: PF00001: 7tm\_1: 1.  
 DR PRINTS: PR00237: GPCPHROPSN.  
 DR PRINTS: PR01012: NEPEPTIDEY.  
 CP P-SITE: PR00237: GPCPHROPSN.  
 KW Neuropeptide.  
 SEQUENCE 375 AA: 42116 MW: 480035511331A1D1 C6064:

Query Match 19.3% Score 368.5: DR 13: Length 375:  
 Best Local Similarity 28.6% Pred. No. 5.3e-22:  
 Matches 94: Conservative 64: Mismatches 18: Indels 5: Gaps 10:

QY 41 PALSALLVLT-----AVDVGNHVIIVISV.PNPKIPNAGNPLVSLADLVVA 90  
 16 PPSANSSSIIFLLVAVSTMLAVSLVNTGLVVTIKKEMPNVNTIFVNAASDILVC 75  
 QY 91 EYPPPLIWAIFDPMALGSEHCKASAFVMSLVYGVFNITAIINRYCYCHSMAYH 150  
 76 LVCLVLIIVILMLRWHIIGALVIVTFVWQMSVTVLISNV:AIHHHIIHPTWKP 135  
 QY 151 IYPPHPTPLHICILMLTVALLP-----NFWVSELYPPYSLFICIAST 103  
 136 VVR-HSYLAVAVIMILACEISLEPFSNITNSPFSNLSLPPNP-FSDHFIIPQWPS 133  
 QY 144 QIASGVTAAYVHIFLLPIVAVSCYPIRWIVVQAPPAKPPESLGLKPSDLPSFT 133  
 132 ENRPLVITILLDQYCIPLALIVYFFIFLPSKRWEPAPQGRKAKSSK 246  
 QY 243 KPSDLPSEFLMEVVFVFAICWAPLNCIGLAVAINPQEMAPQIEGLVTSYLLAVNSG 302  
 242 ---VNAMASTV-AAVLLQWPLVAVNITFEKNHRAIVQGHAIKFSCHLIAMASIC 302  
 QY 303 LNAIVYGLNQNFRPPYKPL--IALNMP 329  
 303 VNPVYIGFLNNPKKIKSLISPPRWSP 331  
 DB 303 VNPVYIGFLNNPKKIKSLISPPRWSP 331

RESULT 12  
 09011 PRELIMINARY: PRT: 388 AA.  
 ID 09011  
 DI 01-MAY-2000 (TREMblrel. 13, Created)  
 DI 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DI 01-JUN-2000 (TREMblrel. 14, Last annotation update)  
 DE D3753D10.1 (SOMATOSTATIN RECEPTOR 4).  
 GN SSTR4.  
 OS Homo sapiens (Human).  
 OC Eukaryota: Metazoa: Chordata: Cranialia: Vertebrata: Euteleostomi:  
 NC Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.  
 NCRI\_TaxID=9606:



Subtype in the zebrafish.  
 RI Biochem Biophys Res Commun 241:749-754(1997)  
 DE EMBL: AF037401.9 AAC41277.1  
 DE ZFIN: ZDB-GENE-990415-175; npryrc.  
 DR INTERPRO: IPR000276  
 DR INTERPRO: IPR000611  
 DR PFAM: PF00001.7tm1.1  
 DR PRINTS: PR00237. GPCRHD00SN  
 DR PRINTS: PR01012. NPEPTIDFR  
 DR PROSITE: PS00237\_5. PROTEIN\_RECEPTOR\_UNKN\_WN\_1  
 KW Neuropeptide  
 SC SEQUENCE 373 AA: 41673 MW: 2170475.64 GPC64:  
 Query Match 17.5% Score 333 DB 13 Length 773  
 Best Local Similarity 27.8% Pred. No. 3,76-19  
 Matches 24 Conservative 64 Mismatches 116 Indels 64 Gaps 13  
 QY 31 SRPPPPWV-----APALS-AVLIV-----TADVVSGLVLSVLRPKLRKLNQNLFC 79  
 DB 10 SCGGGKSWESVNPSPVSTLLIIVASTVAVSLVNTGCTIISPKRHNVTN111 69  
 QY 80 VSLALDLVAEFPYLLIIVAFYDGMALGDECHKASAFVMSVIGSVENITAIANKY 139  
 DB 70 ANSCSDILMCVQCPVTVITIMDRMLICETICKYTPVQCKSVISFSLVTALEKH 129  
 QY 140 CYCHSMANVRIYRW-----HTPHCTIMDLTVALLP-----NEFVS-----SLEVD 184  
 DB 130 QITHTDTS-----WTFPAKSHYIAVAATVMWAGFSLPFLSNLTAPQGNLEPEN 182  
 QY 185 PRYSSTPI-----STASTQYAAVVVITRTIYAVVSFYLRVW-----LVQDA 230  
 DB 163 FSHSHVIMCEWSEKPLAVTISTILFVCTITLILLYLPFLLEPKRWNSA 24  
 QY 231 ----PRKAPESPLCLKPSDLSEFLTFEVFVI-FAICMAPLNCIGLAIVAPQEMAPQI 285  
 DB 241 TAPKPKKAGAGV-----NMLVYIVAFNLEMLFNVTITKWHLLIAQ 293  
 QY 286 PRGPTVSTVLLAFNGCLNAIVGILNCPPEYKPL 223  
 DB 291 HDVIFACHLTMASTGVNVYVGFENFQKELKATL 328  
 RESULT 15  
 Q9K498  
 AC Q9K498 PRELIMINARY PRI: 386 AA  
 DT 01-MAY-2000 (TREMBL) 13 Created  
 DT 01-MAY-2000 (TREMBL) 13 Last sequence update  
 DT 01-JUN-2000 (TREMBL) 14 Last annotation update  
 DE G33171 PROTEIN.  
 GN G33171  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydridae; Ephydrididae; Ephydridia  
 OC NCBI\_TaxID=7227  
 RN 11  
 RP SEQUENCE FROM N.A.  
 TC STRAIN=REKRELEY  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M D, Gelinkler S F, Holt P A, Evans C A, Gocayne J L,  
 RA Amaralides P G, Scherer S E, Li P W, Hoskins R A, Galie R F,  
 RA George R A, Lewis S B, Richards S, Ashburner M, Henderson S N,  
 RA Sutton G G, Wortman J R, Yandell M D, Zhang Q, Chen L X,  
 RA Brandon R C, Rogers Y H, Blazer V C, Chapple M, McEwen R D,  
 RA Wan K H, Doyle C, Baxter F G, Holt G, Nelson C P, Miklos G L G,  
 RA Abul J F, Adhyan A, An H T, Andrews-Pfannkoch C, Baldwin D,  
 RA Ballew F M, Basu A, Baxendale J, Bayraktarolu L, Beasley E M,  
 RA Beeson K Y, Bencze P V, Bereman D P, Bhattacharya D, Bolduc E J,  
 RA Botvina D, Botchan M P, Bouck J, Brockton P, Brockton P,  
 RA Burks K C, Busan D A, Butler H, Cadieu E, Center A, Chandra T,  
 RA Cherry J M, Cawley S, Dahlke C, Davenport L B, Davies P,

De Fabios B, Delcher A, Deng Z, Mays A D, Fowler I, Dietz S M,  
 RA Enderson K, Dong L E, Donnes M, Engan-Kocha S, Enkav H O, Dunn P,  
 RA Durbin K I, Evangelista C, Ferrar G, Ferreira S, Fleishmann W,  
 RA Foster C, Gabriellian A E, Gary N S, Gelbart W M, Glasser K,  
 RA Glodde A, Gong F, Gorrell J H, Gu Z, Guan P, Harris M,  
 RA Harris N L, Hargrey D, Helman T, Hernandez P, Houck J,  
 RA Hostin D, Houston K A, Howard T, Wei M H, Ibbam C,  
 RA Jialit M, Kluge E, Kaffen G H, Ke Z, Krontz T A, Krontz X A,  
 RA Kralik P, Kralik C, Kraft C, Krawiec S, Kuhl D, Lee Z,  
 RA Lasko J, Lee V, Levinsky A A, Li T, Li T, Liang Y, Lin X,  
 RA Liu X, Mattei R, McIntosh T C, McLeod M P, McPherson D,  
 RA Merkulov G, Mikhina N V, Moatry C, Morris I, Mostrelli A,  
 RA Mount S M, Moy M, Murphy B, Murphy L, Muzny D M, Nelson D L,  
 RA Nelson D P, Nelson K A, Nixon K, Nusskern D P, Pachter J M,  
 RA Palazzolo M, Pittman G S, Pan S, Pollard T, Puri V, Reese M,  
 RA Palzer K, Penington K, Saunders P D, Schaefer F, Shen H,  
 RA Shaw E, Shih-Klaus I, Simpson M, Skusek M P, Smith T,  
 RA Spier E, Spradling A C, Stapleton M, Strong P, Sun E,  
 RA Svrtkav P, Tector C, Turner R, Venter E, Wang A H, Wang X,  
 RA Wang Z Y, Wasserman D A, Weisslock G M, Weissbach J,  
 RA Williams S M, Woodage J, Worley K C, Wu P, Yang S, Yao Q A,  
 RA Ye J, Yeh P F, Zaveri J S, Zhan M, Zhan G, Zhao G, Zheng L,  
 RA Zheng X H, Zhong F N, Zhong W, Zhou X, Zhu S, Zhu X, Smith H O,  
 RA Gibbs R A, Myers E W, Rubin G M, Venter J C;  
 RI The genome sequence of Drosophila melanogaster;  
 RL Science 297:124-129(2000).  
 DR EMBL: AF004351. AAF4609.1  
 DR FLYBASE: FBgn0029786; CG3171.  
 DR INTERPRO: IPR000276; 1  
 DR PFAM: PF00001.7tm1.1  
 DR PRINTS: PR00237. GPCRHD00SN  
 DR PROSITE: PS00237\_5. PROTEIN\_RECEPTOR\_1  
 DR SC: 386 AA: 41673 MW: 2170475.64 GPC64:  
 Query Match 17.5% Score 333 DB 5 Length 386  
 Best Local Similarity 26.0% Pred. No. 3,76-13  
 Matches 97 Conservative 67 Mismatches 158 Indels 42 Gaps 12  
 QY 27 SAPSPPTPPPPWPAALSAVITVAVDGNLVLISVLPKRP-NAGNFIASIA 95  
 DB 18 AATQISPHSATLEFALISACVFT--IGVGNITLILKSPITREHATVIAISIS 75  
 QY 86 ELVAFYPRYLIVATYTESMALGDECHKASAFVMSVIGSVENITAIANKY-CH 144  
 DB 76 CLPQSESIPIAVPRQPSWTFPIITRTFVTFGNVAVSI SWAGTINPYLIAOH 135  
 QY 145 SMAHPIYPPWHTPLHLCILMITVVAIPNF--FVSTFEDPRIVSCFTQVATYA 202  
 DB 136 S-RVSCIVPRFTLLIFVWASVFLLEPTITGVFMRTATFQITIKVPSISIK 194  
 QY 203 AVVAVPELIVAVSPSYRTFWVIQAPK-----AKPS-----PCT 242  
 DB 135 TLFVZCLFLVAVVSVSTIVVHKKFIRHNF--FAVAV--SSSSSTGVWTTT 254  
 QY 243 KPS--ELPSFLIMVAVVIFALMAHLNCLGLAVAINQEMAVQIEGJLVSYLLAYN 300  
 DB 265 EKAEINPLIVAVITFLCLVCTIF-----KAVNVDERTSTP-WCHTASVAKAS 309  
 QY 301 SCLNAVYGLNCPPEYKPL--LLALMN-----FHHIQDASGSHAFQSPAPPI 352  
 DB 310 SVNMLIVYANNNHVVAVYKILLALKFWCEPLSPKSSGVHVS<NSKRTSVTSTPTF 369  
 QY 353 IGVD 356  
 DB 370 HAVQ 373

Search completed: February 15, 2001, 16:45:34  
 Job time: 9252 sec

Tue Feb 20 11:43:02 2001

us-09-226-046-16.rspt

---

Page 8







PD 23-DEC-1995.  
 XX  
 PF 07-JUN-1995: 05MO-0507360  
 XX  
 PR 06-JUN-1995: 9505-0319687.  
 XX  
 PR 17-JUN-1994: 9405-0261857.  
 PR 07-OCT-1994: 9405-0319687.  
 XX  
 PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
 XX  
 PI Reppert SM.  
 XX  
 DR WPI: 1996-058368/06.  
 DR N-PSDB: T09952.  
 XX  
 PT DNA encoding high affinity melatonin receptor one - used to identify  
 PT receptor agonists or antagonists e.g. for regulating circadian  
 PT rhythm disorders or reproductive cycles  
 XX  
 PS Claim 10: Fig 6: 115pp: English.  
 XX

The sequence represents a novel human high-affinity melatonin-1b receptor (mol.wt. 40,188), which is a membrane protein, coupled to guanine nucleotide binding proteins (G-proteins), with 7 hydrophobic putative transmembrane domains. Unique features of 1b receptors include an NRY motif downstream from the 3rd transmembrane domain, and an NAXY motif in transmembrane-7, rather than NPXXY. A CYCHS motif, which is a consensus site for cytochrome-c family heme binding, is present in both 1b and 1a-type receptors. The N-terminus contains 1 consensus N-glycosylation site. Receptor fragments which interact with melatonin, or specific antibodies, may be used as receptor-agonists or receptor-antagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonal breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic animal for use as a model system to screen agonists and antagonists.

Sequence 362 AA:

Query Match 59.3% Score 1088: DR 17: Length 362:  
 Best Local Similarity 61.2% Pred. No. 1,1e-109:  
 Matches 205: Conservative 5.7: Mismatches 70: Indels 8: Gaps 1:

QY 2 GNGSALPNASCPVLPGGGAPPSWLASA:AVV:FTIVVRI/GNLTIVTSVPRKKEFNAG 62  
 Db 24 qasasrpart-----prppwapsalsavllvtadvgvgnllvltvlnrklnag 75  
 QY 63 NLFVSLVAALVAIVAVPYPLVMSIFNNQWNLGVLCQVSGFMGSLVSGISFNITGIA 122  
 Db 76 NLFVSLVADLVAVVGYPLVMSIFNNQWNLGVLCQVSGFMGSLVSGISFNITGIA 135  
 QY 123 INRYCYCHSLKCYKLSKNSICVYLILWLTCAVLPNLSAGTLCAYDPRIYCTAGS 182  
 Db 136 INRYCYCHSLKCYKLSKNSICVYLILWLTCAVLPNLSAGTLCAYDPRIYCTAGS 195  
 QY 183 VSSATTIAVVFHFLVPMIVIFCYLRTWILVQVRCVNRKDFKPKKQCFRNTVMFY 242  
 Db 196 astgtaavvvvhlilpavvsfcyrltwlvlgtrfrakpessiclkfssdlstlmtlv 255  
 QY 243 VFVLEIAQMAFLNFTGLAVASDFASMPRIPEMLFVASYVATVNSCANAIVQLNQNF 302  
 Db 256 vfvleiaqmaflnftglavasdffasmpripemlfvasyvatvnsccanaivqlnqnf 315  
 QY 303 KREYRIIVSLCIAVFEVDSNEMALVYNNKPSF 337  
 Db 316 treykrillalwmpfclqdaekqshaeqldgspap 350

RESULT 12

Y45129  
 ID Y45129 standard; Protein; 346 AA.

XX  
 AC Y45129;

XX  
 DT 21-DEC-1999 (first entry)

XX  
 DE Rat galanin receptor 1.

XX  
 KW Physiologically active peptide; receptor binding; galanin receptor;  
 KW GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin;  
 KW drug development; memory function; appetite improver; womb; kidney;  
 KW function regulator; prostate; testis; skeletal muscle.

XX  
 OS Rattus sp.

XX  
 PN W09948920-A1.

XX  
 PD 30-SEP-1999.

XX  
 PF 24-MAR-1999: 99MO-JP01482.

XX  
 PR 25-MAR-1998: 98JP-0078139.

XX  
 PR 21-SEP-1998: 98JP-0266972.

XX  
 PA (TAKA) TAKEDA CHEM IND LTD.

XX  
 FI Chitaki T, Matsui H, Ishibashi Y, Ogi K, Kitada C.

XX  
 DR WPI: 1999-572170/48.

XX  
 DR N-PSDB: 225518.

XX  
 PT peptides binding to galanin receptor proteins, used to, e.g. improve  
 PT kidney functioning.

XX  
 PS Claim 1: Page 119-121; 153pp: Japanese.

The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APARRRG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. Y45129 to Y45134 and 225518 to 225552 represent sequences used in the exemplification of the present invention.

Sequence 346 AA:

Query Match 18.7% Score 340: DR 20: Length 346:  
 Best Local Similarity 29.3% Pred. No. 1,1e-28:  
 Matches 96: Conservative 67: Mismatches 123: Indels 42: Gaps 11:

QY 2 GNGS ALPNASCPVLPGGGAPPSWLASA:AVV:FTIVVRI/GNLTIVTSVPRKKEFNAG 56  
 Db 10 eqnsgdeppaaprpilgfy.....venfctivfgltfagvlgnsilvltvlnrkspg 63

QY 57 KLEPMAGNIFVSLAVANLVAVPYPLVMSIFNNQWNLGVLCQVSGFMGSLVSGISIF 116  
 Db 64 kpeetmllflgslstddlyllfclpfglvvlpfwtvlgatctgfyftvsmvssif 123

QY 117 NITGIAINPYVYCHSLKCYKLSKNSICVYLILWLTCAVLPNLSAGTLCAYDPRIY 175  
 Db 124 tlaamsvdyvvalvhsrresslrvetnallgvgfltwalslmasp-----vayvtrflth 177

QY 176 .....SCTEA.....QSSVATTIAVVFHFLVPMIVIFCYLRTWILVQVRCVNRKDFKPKKQCFRNTVMFY 226  
 Db 178 rdsnqclfcwehpnqllhkkayvclftvgyllpllllclcykav---lnhllkklk-nms 233

QY 227 PKLKPQDFRNFVIMFVFLFAICWALNFIQL....AVASDPKSMWRPIPEMLFVASY 281  
 Db 227 PKLKPQDFRNFVIMFVFLFAICWALNFIQL....AVASDPKSMWRPIPEMLFVASY 281

```

FT      152..171          *transmembrane domain 4*
ET      172..194          *extracellular domain 3*
ET      194..219          *transmembrane domain 5*
ET      220..244          *intracellular domain 3*
ET      244..268          *transmembrane domain 6*
ET      269..280          /note= "extracellular domain 4"
ET      281..301          /note= "transmembrane domain 7"
ET      302..354          /note= "intracellular C-terminal domain"
FN      W09704D094.A1.
XX
XX      06-FEB-1997.
XX
XX      24-JUL-1996;          96WD-FR01167.
XX
XX      24-JUL-1995;          96FR-0000947.
XX
XX      (ADP ) ADP 5 01E.
XX
XX      Dockers R. Marullo S. Stosberg AD;
XX
XX      WP1: 1997-132635/12
DB      N-PSDR: T79065-6.
XX
XX      Now nucleic acid encoding functional melatonin receptor of Xenopus -
PT      for screening for potential (anti)agonists useful for e.g. treating
PT      cardiovascular disease and cancer
XX
XX      Claim 5; Page 30-31; 62pp; French.
XX
XX      Sequences W57977 represent novel allelic Xenopus laevis melatonin
XX      receptor MEL-1A proteins. This sequence is a new form of the melatonin
XX      receptor designated MEL-1AB, also known as Mel 1-(beta). The protein
XX      differs from previously known receptors by being 65 amino acids shorter
XX      and also differs throughout the sequence by 6 amino acids. The protein
XX      is encoded by 2 different alleles (T79065-6) which differ in the 3'
XX      untranslated region (both sequences encode the same protein), which is
XX      thought to affect the half-life of the mRNA. The coding sequence was
XX      isolated from cDNA derived from Xenopus skin RNA and amplified using the
XX      primers 17927-77. The nucleotide sequence encodes a 7 transmembrane
XX      receptor involved in cellular signalling. MEL-1AB has been shown to
XX      mediate intracellular comp. esp. inhibiting its accumulation induced by
XX      an inhibitor of phosphodiesterase, but unlike the MEL-1AA protein, it
XX      cannot inhibit adenylyl cyclase activity.
XX
XX      Sequence: 154 AA.
XX
Query Match:           68.3% Score 1240. DP 18 Length 154
Post Local Similarity: 70.4% Prot No. 3 Seq 126
Matches: 221 Conservative: 521 Mismatches: 421 Indels: 0 Gaps: 0
25  LASALACVLETFIVYIGLNLVLVSYYNKKLFKNGNIPVYSLAAGLVAVIPEVLT 95
26  LLLLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
26  ILSALAYIIIIIVDVLIIMILVILSVLENKLQNAQGLFVSLSLADLVATVYPPII 90
45  MSIFNNKNKLYTHRGVSRFLMGSLVSGISLNITGIAIPRYCYFGSTFYVYSSKNSI 145
46  ILLIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
46  IALLIQAWEIHLNHQSISLIIMLVISGVFIITALAIRYICHSIYLKDLIRISTW 150
46  QVALIIMILLITAAVPINPLFACTLOVEPRYSSTPAQSVSAATIAVVHRELVPMIIV 205
46  IYNIATKRIIILAIIPAILVASIIYDFITSCSTLAFQSSSYTLIDVRRHHIAPSLVCF 210
46  CYIRIWLIVLGVRGVRKHDKRKIKLPDGFENFVTEFEVVFALCAICAPINLTGLAVASDP 265

```

[illegible]

FT	Domain	/note= "Protein-kinase-C phosphorylation site"
FT	Domain	152..171
FT	Domain	/note= "Transmembrane region-IV"
FT	Misc-difference	166
FT	Domain	/note= "Residue which may form ligand binding pocket"
FT	Domain	172..193
FT	Domain	/note= "Extracellular loop"
FT	Domain	194..229
FT	Domain	/note= "Transmembrane region-V"
FT	Misc-difference	204
FT	Domain	/note= "Residue which may form ligand binding pocket"
FT	Domain	221..243
FT	Domain	/note= "Intracellular loop"
FT	Domain	244..268
FT	Domain	/note= "Transmembrane region-VI"
FT	Region	252..259
FT	Domain	/note= "Region used to construct primer"
FT	Misc-difference	258
FT	Domain	/note= "Residue which may form ligand binding pocket"
FT	Domain	269..279
FT	Domain	/note= "Extracellular loop"
FT	Domain	280..301
FT	Domain	/note= "Transmembrane region-VII"
FT	Region	296..300
FT	Domain	/note= "Conserved melatonin receptor-1b motif"
FT	Domain	302..420
FT	Modified-site	/note= "Intracellular domain"
FT	Modified-site	320
FT	Modified-site	/note= "Protein-kinase-C phosphorylation site"
FT	Modified-site	328
FT	Modified-site	/note= "Protein-kinase-C phosphorylation site"
FT	Modified-site	362
FT	Modified-site	/note= "Protein-kinase-C phosphorylation site"
FT	Modified-site	395
FT	Modified-site	/note= "Protein-kinase-C phosphorylation site"
FT	Modified-site	418
FT	Modified-site	/note= "Protein-kinase-C phosphorylation site"
XX		
XX	W09535320-A1	
XX		
XX	28-DEC-1995	
PD		
XX	07-JUN-1995	95WO-0507360
PE		
XX	06-JUN-1995	95US-0319887
PR	17-JUN-1994	94US-0261857
PR	07-OCT-1994	94US-0319887
XX		
XX		
PA	(MASS-) MASSACHUSETTS GEN HOSPITAL	
PI	Reppert SM	
XX		
DR	WPI: 1996-058368/05	
DR	N-PSDB: 109947	
XX		
PT	DNA encoding high affinity melatonin receptor one - used to identify	
PT	receptor agonists or antagonists e.g. for regulating circadian	
PT	rhythm disorders or reproductive cycles	
XX		
PS	Claim 5: Fig 1: 115pp: English	
XX		
CC	The sequence represents a high-affinity melatonin receptor (mol.wt.	
CC	47,442) from <i>Xenopus laevis</i> . The receptor is a membrane protein,	
CC	coupled to guanine nucleotide binding proteins (G-proteins) and	
CC	has 7 hydrophobic putative transmembrane domains. The N-terminus	
CC	has an N-linked glycosylation site typical for G-protein-coupled	
CC	receptors, and 2 Cys residues in the 1st 2 extracellular loops may	
CC	form a stabilizing disulfide bond. Pro residues in transmembrane	
CC	domains IV, V and VI may introduce kinks in the alpha-helices to	
CC	form of a ligand binding pocket. Phosphorylation sites in the	
CC	C-termini may be involved in receptor regulation. Primers from the	
CC	encoding DNA may be used for isolation of sheep, mouse and human	
CC	receptor sequences. Receptor fragments which interact with	

CC melatonin, or specific antibodies, may be used as receptor-agonists  
CC or receptor-antagonists. Acronists may be used in therapy of  
CC circadian rhythm disorders such as jet-lag or day-night cycle  
CC disorders, to control ovulation, or in alteration of reproductive  
CC cycles in seasonally breeding animals. Antagonists may be used to  
CC control the initiation or timing of puberty in humans. The  
CC receptor gene may also be expressed in a transgenic animal for use  
CC as a model system to screen agonists and antagonists.  
XX  
SQ Sequence 420 AA:

Query Match	68.5%	Score 1244;	DB 17;	Length 420;
Best Local Similarity	70.4%;	Pred. No. 1 6e-126;		
Matches 224, Conservative	52;	Mismatches 42;	Indels 0;	Gaps 0.

Qy	28	LASADLAAVLIIIVLIDGSLVLVLSL	ENRRLALENGAIIIVLSRAVDLVAIIIVL	28
Db	31	ltsalavlllftvdvdlgrlllvstlrkkk	lqnaaillvyslslldlvvaayfpvll	90
Qy	86	MSIRNNGNIIQYLCQVSGFMCLSTVGSIFENIGIAINRCYICGELKRYDKYSSKNSL		145
Db	91	laifqngkltlnihcqsqglimgslsvsgvsnltataltmcyichslrydklyngqstw		150
Qy	146	CYVLLIMLITLAAVLEFLNRAGTLODYDFRZYSCFPAQSSASATTAAYVPHFLVPMIAVIF		205
Db	151	Cyglftwlltlllavprftfvygslgyhdpifscctlaqvssgyltvayvvllyflvskwelf		210
Qy	206	CYIFRMITVLIDVQPPVPRPRPKPKRQCPFNFTMFEVFLPAICMAFLNFTIGLAVASCP		265
Db	211	Cyfltkwvlyqpkrtvvgqslgkrltgqcdltlrltlmrtvrlfllsrgapnllflqjrtllcp		270
Qy	266	ASMWPIPIFEMIIFVASIYMAVFNSGLNIIYQILNQNFRFVSPPIIVSLVTAAPVFVNDSSN		325
Db	271	fwagpklpowlfvrlsyymaynsnclnavlvevllqgclrfvaykrlmsllprllfjtdtstr		330
Qy	326	DVADVPRKKRPSPLMTNNN	343	
Db	331	gqtqglkkspspavltinn	348	

RESULT	10
ID	W25927
AC	W25927 standard; Protein; 354 AA.
NC	W25927;
DI	10-NOV-1997 (first entry)
XX	Xenopus melatonin receptor MEL-1A.
DE	
XX	Allele: Xenopus laevis; melatonin; receptor; untranslated region; PCR:
KW	mRNA; half-life; skin; amplification; primer; polymerase chain reaction;
KW	transmembrane domain; cellular signaling; inhibition; adenylyl cyclase;
KW	modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase.
XX	
OS	Xenopus laevis.
XX	
FH	Key
FT	Location/Qualifiers
FT	1..32
FT	/note= "Extracellular N-terminal domain"
FT	33..56
FT	/note= "transmembrane domain 1"
FT	57..68
FT	/note= "intracellular domain 1"
FT	69..92
FT	/note= "transmembrane domain 2"
FT	93..107
FT	/note= "extracellular domain 2"
FT	108..125
FT	/note= "transmembrane domain 3"
FT	126..151
FT	/note= "intracellular domain 2"

Accession	Protein	Location	Notes
U00001	Protein	1-32	Location: "Cell Surface"
U00002	Protein	33-56	Location: "Extracellular N-terminal domain"
U00003	Protein	57-68	Location: "Transmembrane domain 1"
U00004	Protein	69-92	Location: "Intracellular domain 1"
U00005	Protein	93-107	Location: "Transmembrane domain 2"
U00006	Protein	108-125	Location: "Extracellular domain 2"
U00007	Protein	126-151	Location: "Transmembrane domain 3"
U00008	Protein	152-171	Location: "Intracellular domain 2"
U00009	Protein	172-193	Location: "Transmembrane domain 4"
U00010	Protein	194-219	Location: "Extracellular domain 3"
U00011	Protein	220-243	Location: "Transmembrane domain 5"
U00012	Protein	244-268	Location: "Intracellular domain 3"
U00013	Protein	269-280	Location: "Transmembrane domain 6"
U00014	Protein	281-301	Location: "Extracellular domain 4"
U00015	Protein	302-354	Location: "Transmembrane domain 7"
U00016	Protein	355-380	Location: "Intracellular C-terminal domain"

	Melatonin	26	TASALAGVITFTIVVOIGLGNLLVLISVRNKKRLPACNIPIVSGAVADLVAAIPHYPLV	85
C7		26		
Lb		31	ltsalavvllftivdvvglnltvlstvrnkkgaaqlfvsqsladlvayafypvll	90
Cy		26	MSLFNNMNLVCLPHVNSFLMRSVGISFENTICIAINPCYVCHSPKVIYSRPSL	145
Lb		31	latifgngltglahoglsqilmgletsvssvtoltalanrfeychslrydklprgqrll	150
Cy		146	GVVLTWMLTAAVLPNTPACTGYPDPVYSTENQGSVSATTAVVHFHPVPIVIF	205
Lb		151		
C7		206	GILRFIVIVGVPGVKRDPRPKLRPOFPNVNPVFVVPVPAIOWAPINTSLAVASDP	265
Lb		211		
Cy		266	ASMWRPFEMTLFVASVYMAFYNSCLNALITYELNMFREKEYEPVIVSLCAKAFVFSNN	325
Lb		271		
C7		326	DVADRVKKRPSPPLMTNNN	343
Lb		331	qtetgkkspspavtmn	348
RESULT		9		
ID	P88409			
XX	P88409 standard: Protein; 420 AA.			
AC	R88409:			
XX	15-AUG-1996 (first entry)			
DI				
XX				
DE	High-affinity melatonin receptor.			
XX				
KM	Melatonin receptor; G-protein-coupled receptor; glycosylation;			
KM	disulfide bond; ligand binding pocket; phosphorylation;			
KM	cyclochrome-c family heme binding site; melatonin receptor-agonist;			
KW	melatonin receptor-antagonist; circadian rhythm disorder; jet-lag;			
KW	day-night cycle disorder; ovulation; reproductive cycle; antibody;			
XX	animal breeding; puberty; transgenic animal; drug screening.			
OS	Xenopus laevis.			
XX				
Key	Location/Qualifiers			
FT	Domain	1..32		
FT	/note= "Extracellular domain"	5..7		
FT	Modified-site	/note= "N-glycosylation site"	16	
FT	Modified-site	/note= "Protein-kinase-C phosphorylation site"	33..57	
FT	Domain	57..68		
FT	Domain	69..93		
FT	Region	94..107		
FT	Region	108..126		
FT	Disulfide-bond	127..151		
FT	Domain	152..182		
FT	Domain	183..213		
FT	Region	214..244		
FT	Domain	245..275		
FT	Domain	276..306		
FT	Region	307..337		
FT	Region	338..368		
FT	Region	369..399		
FT	Region	400..430		
FT	Region	431..461		
FT	Region	462..492		
FT	Region	493..523		
FT	Region	524..554		
FT	Region	555..585		
FT	Region	586..616		
FT	Region	617..647		
FT	Region	648..678		
FT	Region	679..709		
FT	Region	710..740		
FT	Region	741..771		
FT	Region	772..802		
FT	Region	803..833		
FT	Region	834..864		
FT	Region	865..895		
FT	Region	896..926		
FT	Region	927..957		
FT	Region	958..988		
FT	Region	989..1019		
FT	Region	1020..1050		
FT	Region	1051..1081		
FT	Region	1082..1112		
FT	Region	1113..1143		
FT	Region	1144..1174		
FT	Region	1175..1205		
FT	Region	1206..1236		
FT	Region	1237..1267		
FT	Region	1268..1298		
FT	Region	1299..1329		
FT	Region	1330..1360		
FT	Region	1361..1391		
FT	Region	1392..1422		
FT	Region	1423..1453		
FT	Region	1454..1484		
FT	Region	1485..1515		
FT	Region	1516..1546		
FT	Region	1547..1577		
FT	Region	1578..1608		
FT	Region	1609..1639		
FT	Region	1640..1670		
FT	Region	1671..1701		
FT	Region	1702..1732		
FT	Region	1733..1763		
FT	Region	1764..1794		
FT	Region	1795..1825		
FT	Region	1826..1856		
FT	Region	1857..1887		
FT	Region	1888..1918		
FT	Region	1919..1949		
FT	Region	1950..1980		
FT	Region	1981..2011		
FT	Region	2012..2042		

```

Db 194 Lfsgvssaytlavvvfhf.vpm.lvfwfvyll:lwai.vjvfwkvkpdnkpklhpqalf: 253
QY 238 VTMEVVEVLAICMAPLNF:GLAVASDPASMPVPRIPEMLFVASVYMAVENSCINAIYGT 297
Db 254 vtmevvevleicmaplnf:glavasdpasmpvpripemlfvasvymayfasc:naiiygt 313
QY 298 LNCNFKPKPRRIIVSCTAPVFEVDSNVADPVKWKPKPSPLMTNNNVKVDV 350
Db 314 lncnfkprkprriivsctapvfevdsnvadpvkwwkpsplmtnnnvkvds 366

RESULT 7
R88411
ID R88411 standard: Protein: 288 AA.
XX
XX R88411:
XX
XX 16-AUG-1996 (first entry)
XX
DE High-affinity melatonin-1a receptor fragment.
XX
KW Melatonin-1a receptor; human; G-protein-coupled receptor;
KW cytochrome-c family heme binding site; antibody;
KW melatonin receptor-agonist; melatonin receptor-antagonist;
KW circadian rhythm disorder; jet-lag; day-night cycle disorder;
KW ovulation; reproductive cycle; animal breeding; puberty;
KW transgenic animal; drug screening.
XX
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..2 /note= "Intracellular loop fragment"
FT Region 1..6 /note= "Conserved melatonin receptor motif"
FT Domain 3..27 /note= "Transmembrane region-II"
FT Domain 28..41 /note= "Extracellular loop"
FT Domain 42..50 /note= "Transmembrane region-III"
FT Domain 51..85 /note= "Intracellular loop"
FT Region 66..71 /note= "Putative cytochrome-c family heme binding site"
FT Domain 86..114 /note= "Transmembrane region-IV"
FT Domain 105..126 /note= "Extracellular loop"
FT Domain 127..153 /note= "Transmembrane region-V"
FT Domain 154..176 /note= "Intracellular loop"
FT Domain 177..201 /note= "Transmembrane region-VI"
FT Domain 202..212 /note= "Extracellular loop"
FT Domain 213..234 /note= "Transmembrane region-VII"
FT Region 229..233 /note= "Conserved melatonin receptor 1a motif"
FT Domain 235..288 /note= "Intracellular domain"
XX
XX W0955320-A1.
XX
XX 28-DEC-1995.
XX
XX 07-JUN-1995: 95W0-US07350.
XX
XX 06-JUN-1995: 95US-0319887.
XX
XX 17-JUN-1994: 94US-0261857.
XX
XX 07-OCT-1994: 94US-0319887.

```

```

XX
XX (MASS-) MASSACHUSETTS GEN HOSPITAL.
XX
XX Repeat SM:
XX
XX WPI: 1096-058366/06
XX
XX N-PSNR: 109949.
XX
XX DNA encoding high affinity melatonin receptor cDNA used to identify
XX receptor agonists or antagonists e.g. for regulating circadian
XX rhythm disorders or reproductive cycles
XX
XX Claim 7; Fig 4; 115pp; English.
XX
XX The sequence represents a fragment of a human high-affinity
XX melatonin-1a receptor, which is a membrane protein, coupled to
XX guanine nucleotide binding proteins (G-proteins), with 7
XX hydrophobic putative transmembrane domains. The full-length
XX sequence is given in R88412. Receptor fragments which interact
XX with melatonin, or specific antibodies, may be used as
XX receptor-agonists or receptor-antagonists. Agonists may be used in
XX therapy of circadian rhythm disorders such as jet-lag or day-night
XX cycle disorders, to control ovulation, or in alteration of
XX reproductive cycles in seasonally breeding animals. Antagonists
XX may be used to control the initiation or timing of puberty in
XX humans. The receptor gene may also be expressed in a transgenic
XX animal for use as a model system to screen agonists and antagonists.
XX
XX Sequence 288 AA:
XX
XX Query Match 79.5% Score 1443.5; DB 17; Length 288;
XX Best Local Similarity 96.0%; Proj No 24e-148.
XX Matches 280; Conservative 1; Mismatches 7; Indels 1; Gaps 1;
XX
XX QY 62 GNIFVSLAVADLVAIAIPYPLVLSIFNMGNIQYLHCQVSGFLMGLSVGISFNTIGI 121
XX |||||
XX Db 1 gnlfrslavadvlvaiaipypplvlmsifnmgniqylhcgysglmgysglfnitgi 60
XX
XX QY 122 AINPVCYITGSKTKYKLYSKSKNGCYVLLIMLTLAATLPINPACTLOYPRTSCTAQ 181
XX |||||
XX Db 61 ainyrcyltshskckdklyssknslyvllltaaalplrlrtgllyepriysctlaq 119
XX
XX QY 192 SVSASVTIAVVVFHFLVMIIVIPCYLPIWILVLOVPFVDPKPKIKPDPTNFVWF 241
XX |||||
XX Db 120 svssaytlavvvfhf.vpm.lvfwfvyll:lwai.vjvfwkvkpdnkpklhpqalf: 179
XX
XX QY 242 VVEVFLAICMAPLNF:GLAVASDPASMPVPRIPEMLFVASVYMAVENSCINAIYGT 301
XX |||||
XX Db 180 vtfvlfal:ewaplntfiglavsdpsmvpri:powlfrvsgymjyfnscina:egymwgn 239
XX
XX QY 302 PKREPRRIIVSCTAPVFEVDSNVADPVKWKPKPSPLMTNNNVKVDV 350
XX |||||
XX Db 240 fdkgytrilvvlvltavtfvdsndvadvkwkpfplmtnnnvkvds 288
XX
XX RESULT 8
XX W25926
XX ID W25926 standard: Protein: 354 AA.
XX
XX W25926:
XX
XX 10-NOV-1997 (first entry)
XX
XX Xenopus melatonin receptor MEL-1aa.
XX
XX
XX Allele: Xenopus laevis; melatonin; receptor; untranslated region; PCR;
XX mRNA; half-life; skin; amplification; primer; polymerase chain reaction;
XX transmembrane domain; cellular signalling; inhibition; adenylyl cyclase;
XX modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase.
XX
XX Xenopus laevis.
XX
XX OS
XX

```





```

CC mental confusion.
XX
SQ Sequence 350 AA:

Query Match 100.0% Score 1815, FR 18, Length 350
Best Local Similarity 100.0% Pred. No. 176-188
Matches 150: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 MCGNGSALPNASQPVLPDGGAPPSPWLSALACVLTFTVVDITLGNLTLSVYFNKRLPN 60
DB 1 mqngnsalpnasqpvlpdggappspwlsalacvltftvvditlgnltlsvynkrlpn 60
QY 61 AGNIFVSLAVADLVVAIIPYPLVMSIFNNQNLGYLHCQVSGFLMGLSVIGSFNITG 120
DB 61 agnifvslavadvlvaaiipyplvlmsifnnqnlgylhcvsgflmglsvigsfnitg 120
QY 121 IAINPGCYHSHSKYKPKLSSKNSCYVLLIWLIIAAVLPNIACTCYGPRVYSCFA 180
DB 121 iainpgcyhshskykpklyssknsyvvllilwlilaaavlpniactcygprvyscf 180
QY 181 QSVSSAVTIAVVVPHFLPMIIVFCYLPILWLVLQVPQPKPPKPKLQDDEPNVYM 240
DB 181 qsvssavtiavvvphflpmiivfcylpilmvlvlqvpqpkppkpklddnpvym 240
QY 241 FVVVFLPAICMAPLNFGLAVASDFASWPRPFEMFLFVASYMAYFNSCLMAIIYGLNQ 300
DB 241 fvvvflpaicmaplnfglavasdffaswprpfemflfvasyamayfnsclmaiiy 300
QY 301 NPKREYRPIIVSLCTAPVFEVDSNVADVPVKWPKSPPLMTNNNVKVSU 350
DB 301 npkreyrpiivslctapvfevdsnvadvpkwkpsplmtnnnvkvsu 350

RESULT 3
ID W4761 standard: protein: 350 AA.
XX W4761:
AC
XX
DE 28-Apr-1999 (first entry)
XX
DE Human melatonin receptor protein mel-1a.
XX
KW Melatonin receptor; mel-1a; human; screening; hormone.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 249 /note= "encoded by ATT"
FT Misc-difference 274 /note= "encoded by GAG"
FT
XX
XX E092046-A2.
XX
XX 20-JAN-1999.
XX
XX 19-JUN-1998: 98EP-0111352.
XX
XX 17-JUN-1997: 97JP-0180547.
XX
XX (JGCRP-) JCR PHARM CO LTD.
XX
XX Kera J, Shiono H, Yokoyama T;
XX
XX WPI: 1999-083563/08.
XX
XX N-PSDR: X05747.
XX
XX New melatonin receptor expression cells - useful for screening for
XX human melatonin receptor proteins and agonists and antagonists
XX
XX Examples: Fig 2: 24pp: English.

```

```

XX
CC This represents a human melatonin receptor mel-1a. The invention
CC provides materials for screening for a substance showing affinity for a
CC melatonin receptor protein, which comprises an animal cell containing an
CC expression plasmid for the gene encoding a human melatonin receptor
CC protein. The cells are useful for screening for human melatonin receptor
CC proteins and its agonist or antagonist e.g. hormones and synthetic
CC compounds, by measuring changes in metabolic activity. The recombinant
CC human melatonin receptor protein is useful as it has the same activity as
CC natural human melatonin receptor protein. The new screening method is
CC better than prior art radioimmunoassay techniques at quantitatively
CC determining melatonin, which uses antibodies produced by linking
CC melatonin to a carrier.
XX
SQ Sequence 350 AA:

Query Match 99.6% Score 1808, FR 20, Length 350:
Best Local Similarity 99.4% Pred. No. 16-187:
Matches 348: Conservative 1: Mismatches 1: Indels 0: Gaps 0:

QY 1 MCGNGSALPNASQPVLPDGGAPPSPWLSALACVLTFTVVDITLGNLTLSVYFNKRLPN 60
DB 1 mqngnsalpnasqpvlpdggappspwlsalacvltftvvditlgnltlsvynkrlpn 60
QY 61 AGNIFVSLAVADLVVAIIPYPLVMSIFNNQNLGYLHCQVSGFLMGLSVIGSFNITG 120
DB 61 agnifvslavadvlvaaiipyplvlmsifnnqnlgylhcvsgflmglsvigsfnitg 120
QY 121 IAINPGCYHSHSKYKPKLSSKNSCYVLLIWLIIAAVLPNIACTCYGPRVYSCFA 180
DB 121 iainpgcyhshskykpklyssknsyvvllilwlilaaavlpniactcygprvyscf 180
QY 181 QSVSSAVTIAVVVPHFLPMIIVFCYLPILWLVLQVPQPKPPKPKLQDDEPNVYM 240
DB 181 qsvssavtiavvvphflpmiivfcylpilmvlvlqvpqpkppkpklddnpvym 240
QY 241 FVVVFLPAICMAPLNFGLAVASDFASWPRPFEMFLFVASYMAYFNSCLMAIIYGLNQ 300
DB 241 fvvvflpaicmaplnfglavasdffaswprpfemflfvasyamayfnsclmaiiy 300
QY 301 NPKREYRPIIVSLCTAPVFEVDSNVADVPVKWPKSPPLMTNNNVKVSU 350
DB 301 npkreyrpiivslctapvfevdsnvadvpkwkpsplmtnnnvkvsu 350

RESULT 4
ID W23958 standard: protein: 353 AA.
XX W23958:
AC
XX
DE 06-JUN-1998 (first entry)
XX
DE Mouse melatonin 1a receptor.
XX
XX
KW Melatonin 1a receptor; Mel1a gene; circadian rhythm; puberty;
KW reproductive cycle; jet lag; mouse; 5-protein coupled receptor.
XX
XX Mus musculus.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 4..6 /note= "Asn is N-glycosylated"
FT Modified-site 10..12 /note= "Asn is N-glycosylated"
FT Region 31..55 /label= I
FT /label= I
FT /note= "transmembrane region I"
FT /label= I
FT /label= II
FT /note= "transmembrane region II"
FT Region 106..124

```



FT /note= "Extracellular loop"  
 FT 103..121  
 FT /note= "Transmembrane region-III"  
 FT 122..145  
 FT /note= "Intracellular loop"  
 FT 127..133  
 FT /note= "Putative cytochrome-c family heme binding site"  
 FT 147..165  
 FT /note= "Transmembrane region-IV"  
 FT 166..187  
 FT /note= "Extracellular loop"  
 FT 188..214  
 FT /note= "Transmembrane region-V"  
 FT 215..237  
 FT /note= "Intracellular loop"  
 FT 239..262  
 FT /note= "Transmembrane region-VI"  
 FT 263..273  
 FT /note= "Extracellular loop"  
 FT 274..295  
 FT /note= "Transmembrane region-VII"  
 FT 290..294  
 FT /note= "Conserved melatonin receptor-1a motif"  
 FT 296..350  
 FT /note= "Intracellular domain"

MO9535320-A1.  
 PN 28-DEC-1995.  
 XX 07-JUN-1995: 95W0-0507350.  
 XX 06-JUN-1995: 95US-0319887.  
 PR 17-JUN-1994: 94US-0261857.  
 PR 07-OCT-1994: 94US-0319887.  
 XX (MASS-) MASSACHUSETTS GEN HOSPITAL.  
 PA Reprint SM:  
 PI WPI: 1996-058368/06.  
 DR N-PSDB: T09950.

PT DNA encoding high affinity melatonin receptor one - used to identify  
 PT receptor agonists or antagonists e.g. for regulating circadian  
 PT rhythm disorders or reproductive cycles

PS Claim 8: Fig 5: 115pp; English.

XX The sequence represents a human high-affinity melatonin-1a  
 CC receptor, which is a membrane protein, coupled to guanine  
 CC nucleotide binding proteins (G-proteins), with 7 hydrophobic  
 CC putative transmembrane domains. A partial sequence is given in  
 CC R88411. The N-terminus contains 2 consensus N-glycosylation sites,  
 CC compared to 1 site in the Xenopus receptor (R88409), and the  
 CC C-terminal tail is 65 amino acids shorter. Receptor fragments which  
 CC interact with melatonin, or specific antibodies, may be used as  
 CC receptor agonists or receptor antagonists. Agonists may be used as  
 CC in therapy of circadian rhythm disorders such as jet-lag or  
 CC day-night cycle disorders, to control ovulation, or in alteration  
 CC of reproductive cycles in seasonally breeding animals. Antagonists  
 CC may be used to control the initiation or timing of puberty in  
 CC humans. The receptor gene may also be expressed in a transgenic  
 CC animal for use as a model system to screen agonists and antagonists.

XX Sequence 350 AA:

Query Match 100.0%: Score 1915: DP 17: Length 350.  
 Rest Local Similarity 100.0%: Pred No. 1.7e-186:  
 Matches 350: Conservative 0: Mismatches 0: Indels 0: Gaps 0.

UY 1 MGNUNSAIPNAGQVLEKDGAPPSMLASALACVLEFIVVDILDLVIVYENKLEN 60

Db 1 mgnagsalpnasqvlrvggqarpswlasalacvlefiywdlgrllvlsygrnkvtr  
 UY 61 AGNIFVSLAVADIIVAIPYPLVIMSTFNNQWNLGYLHCQVSGFLMGLSIGIFNIG  
 Ub 61 agnlfvslavadiivaipylvmslfnngvnlgylhqvgqslmgslsvgsifnlg  
 QY 121 IAIHRYCYCHS:KYCKLVSXKNSICVCLILWITLAAV:FNRASTLOTDFR:YNCTA 180  
 Db 121 IAIHRYCYCHSLKYCKLVSXKNSICVCLILWITLAAV:FNRASTLOTDFR:YNCTA 180  
 QY 181 QVSSAVTIAVVFHFLVPMIIVFCPLSMILVLCVPPVKKPKPKPKFPSPVPM 240  
 Db 181 qvsavvtiavvfhlvpmiivfcplsmilvlcvpvkkpkpkpkfpfpvpm 240  
 QY 241 FVYVFLAICWAPLNFGLAVASDPASMPRTPEKLFVASYWATNCSINAIYGLNQ 300  
 Db 241 fvvyflaicwaplnfglavasdpsmprtpeklfvasywatnscinaiyglng 300  
 QY 301 NPREYPPITVSLTAPVPEVGSNPNVADPVYWKPEFLMKNHVVVDSV 350  
 Db 301 npreyppitvsltapvpevgssnpsnvadpvyykpeflmknhvvvds 350

RESULT 2  
 ID W15786 standard; Protein; 350 AA.  
 AC W15786;  
 XX 24-JUN-1997 (first entry)

XX Melatonin receptor protein.  
 DE Melatonin receptor protein.  
 XX Melatonin receptor protein; human; chinese hamster ovary cell; CHO cell;  
 KW jet lag; sleeplessness; seasonal melancholia; Alzheimer's disease;  
 KM dementia; cerebral thrombosis; high blood pressure; cancer; melancholia;  
 KW ovulation regulator; neurosis; mental confusion; glioma; therapy.

XX Homo sapiens.

XX JP09084581-A.

XX 31-MAR-1997.

XX 26-SEP-1995: 95JP-0248177.

XX 26-SEP-1995: 95JP-0248177.

XX (TAKE ) TAKEDA CHEM IND LTD.

XX WPI: 1997-052999/23.

XX N-PSDB: T06593.

PT Recombinant human melatonin receptor protein and (ant)agonists -  
 PT used for treating jet lag, Alzheimer's disease, melancholia,  
 PT neurosis, etc.

XX Claim 2: Page 16: 21pp; Japanese.

XX This sequence represents the human melatonin receptor protein. The DNA  
 CC encoding this sequence is used in an expression vector designated  
 CC PAKKO-Mel187. The expression vector is used to produce the chinese  
 CC hamster ovary (CHO) cells of the invention. The CHO cells express the  
 CC human melatonin receptor protein, and can be used to identify compounds  
 CC (such as agonists and antagonists) having affinity to the receptor. The  
 CC CHO cells can also be used to produce the receptor. The melatonin  
 CC receptor agonist can be used as an agent for preventing or treating jet  
 CC lag, sleeplessness, seasonal melancholia, Alzheimer's disease, dementia  
 CC caused by cerebral thrombosis, various diseases accompanying ageing, high  
 CC blood pressure, cancer, and glioma. The melatonin receptor can also be  
 CC used as an agent for preventing or treating melancholia, neurosis, or

GenCore version 4.5  
Copyright (c) 1993 - 2000 GenCore Ltd

us protein - protein search, using sw model

February 18, 2001 20:19:11 Search time 72.17 Seconds

(without alignments)  
165,828 Million cell updates/sec

us-09-226-046-12

Perfect score: 1815  
Sequence: 1 M00000ALINAC2PHEB00 VAWKPSPLMTNNVWVWVWV 350

Scoring table:  
BLOSUM62  
Gap: 10.0, Expect: 0.5

Searched: 258495 seqs, 410735 residues

Total number of hits satisfying chosen parameters: 26487

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-pr crosslink: Minimum Match: 08  
Maximum Match: 1000  
Listing first 45 summaries

Database: 1

A Geneseq 16:  
1 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
2 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
3 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
4 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
5 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
6 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
7 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
8 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
9 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
10 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
11 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
12 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
13 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
14 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
15 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
16 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
17 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
18 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
19 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
20 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
21 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT  
22 /cmm2\_2/ncdata/geneseq/geneseq/AA1984.DAT

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1815	100.0	350	17	High-affinity mela
2	1815	100.0	350	18	Melatonin receptor
3	1808	99.5	350	20	Human melatonin re
4	1570.5	86.5	351	19	Mouse melatonin 1a
5	1552.5	85.5	351	17	R88418
6	1506	82.5	356	17	R88410
7	1443.5	79.5	288	17	R88411
8	1244	68.5	420	18	W25926
9	1244	68.5	420	17	R88429
10	1240	68.3	354	18	W25927
11	1098	59.3	352	17	R88414
12	140	14.5	445	20	V45124

12	335	18.5	249	15	R79412	Galatin receptor.
14	344	18.4	349	17	R65070	Human galatin rece
15	331	18.2	409	21	R76802	Human MY-V-1 rece
16	341	18.2	420	20	R61458	Human T-tasmembr
17	331	18.2	420	21	R79275	Human neurotrophin
18	340.5	18.2	348	17	R65060	Mouse pancreas bet
19	330.5	18.2	348	17	R61229	Mouse pancreas G-P
20	329.5	18.1	355	17	R61158	Murine mu-subtype
21	328.5	18.1	398	16	R76781	Rat mu opiate rece
22	327.5	18.1	399	16	R71954	Rat mu opiate rece
23	327	18.0	401	21	R68880	A murine mu-opioid
24	325	17.9	391	21	R68985	A murine mu-opioid
25	324.5	17.9	405	16	R62535	Porcine beta2 adre
26	324	17.9	432	21	R62535	Rat mu-opioid rece
27	324.5	17.9	432	21	R62535	Rat mu-opioid rece
28	324.5	17.9	432	21	R62535	Rat mu-opioid rece
29	324.5	17.9	432	21	R62535	Rat mu-opioid rece
30	324.5	17.9	432	21	R62535	Rat mu-opioid rece
31	324.5	17.9	432	21	R62535	Rat mu-opioid rece
32	324.5	17.9	432	21	R62535	Rat mu-opioid rece
33	324.5	17.9	432	21	R62535	Rat mu-opioid rece
34	324.5	17.9	432	21	R62535	Rat mu-opioid rece
35	324.5	17.9	432	21	R62535	Rat mu-opioid rece
36	324.5	17.9	432	21	R62535	Rat mu-opioid rece
37	324.5	17.9	432	21	R62535	Rat mu-opioid rece
38	324.5	17.9	432	21	R62535	Rat mu-opioid rece
39	324.5	17.9	432	21	R62535	Rat mu-opioid rece
40	324.5	17.9	432	21	R62535	Rat mu-opioid rece
41	324.5	17.9	432	21	R62535	Rat mu-opioid rece
42	324.5	17.9	432	21	R62535	Rat mu-opioid rece
43	324.5	17.9	432	21	R62535	Rat mu-opioid rece
44	324.5	17.9	432	21	R62535	Rat mu-opioid rece
45	324.5	17.9	432	21	R62535	Rat mu-opioid rece

#### ALIGNMENTS

1	1815	100.0	350	17	High-affinity mela
2	1815	100.0	350	18	Melatonin receptor
3	1808	99.5	350	20	Human melatonin re
4	1570.5	86.5	351	19	Mouse melatonin 1a
5	1552.5	85.5	351	17	R88418
6	1506	82.5	356	17	R88410
7	1443.5	79.5	288	17	R88411
8	1244	68.5	420	18	W25926
9	1244	68.5	420	17	R88429
10	1240	68.3	354	18	W25927
11	1098	59.3	352	17	R88414
12	140	14.5	445	20	V45124

Tue Feb 20 11:42:54 2001

us-09-226-046-12.ra1

Page 1

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

QM protein - protein search, using SW model

Run on: February 18, 2001, 15:44:54 Search time: 54.19 seconds  
(without alignments)  
116 002 Million cell updates/sec

Title: US-09-226-046-12  
Perfect score: 1815  
Sequence: 1 MCGNSGALPMSQVLEKDS VKNKFSFLMTNNHVVVEEV 350

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Issued Patents, AA.\*  
1: /cgn2.6/ptodata/2/133/55A-COMR.pep.\*  
2: /cgn2.6/ptodata/2/133/55B-COMR.pep.\*  
3: /cgn2.6/ptodata/2/133/55C-COMR.pep.\*  
4: /cgn2.6/ptodata/2/133/55D-COMR.pep.\*  
5: /cgn2.6/ptodata/2/133/55E-COMR.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1815	100.0	350	2	US-08-466-103A-12
2	1808	99.4	353	2	US-08-896-365-6
3	1570.5	86.5	353	3	US-09-280-420-2
4	1552.5	85.5	353	2	US-08-466-103A-14
5	1505	82.3	366	2	US-08-466-103A-4
6	1505	82.3	366	2	US-08-466-103A-7
7	1443.5	79.5	288	2	US-08-466-103A-6
8	1244	68.5	420	2	US-08-466-103A-2
9	1175	64.7	257	2	US-08-896-365-8
10	1088	59.3	362	2	US-08-466-103A-16
11	996	58.2	152	2	US-08-896-365-9
12	337.5	18.6	349	3	US-08-513-974B-343
13	335.5	18.5	348	3	US-08-513-974B-446
14	335	18.5	351	3	US-08-513-974B-344
15	330.5	18.2	348	3	US-08-513-974B-342
16	328.5	18.2	391	2	US-08-466-103A-4
17	328.5	18.1	391	2	US-08-466-103A-3
18	328.5	18.1	391	2	US-08-466-103A-5
19	328.5	18.1	391	2	US-08-466-103A-6
20	328.5	18.1	391	2	US-08-466-103A-7
21	328.5	18.1	391	2	US-08-466-103A-8
22	328.5	18.1	391	2	US-08-466-103A-9
23	328.5	18.1	391	2	US-08-466-103A-10
24	328.5	18.1	391	2	US-08-466-103A-11
25	328.5	18.1	391	2	US-08-466-103A-12
26	328.5	18.1	391	2	US-08-466-103A-13
27	328.5	18.1	391	2	US-08-466-103A-14
28	328.5	18.1	391	2	US-08-466-103A-15

29	322.5	17.8	400	1	US-08-351-473B-5	Sequence 5, Appl1
30	319	17.6	400	4	US-08-896-108-8	Sequence 8, Appl1
31	319	17.6	400	4	US-08-896-108-9	Sequence 9, Appl1
32	313	17.2	367	2	US-08-454-552-4	Sequence 4, Appl1
33	313	17.2	367	2	US-08-454-552-5	Sequence 5, Appl1
34	313	17.2	367	2	US-08-454-552-6	Sequence 6, Appl1
35	312.5	17.2	400	1	US-07-783-602C-1	Sequence 7, Appl1
36	312	17.2	400	1	US-07-783-602C-2	Sequence 8, Appl1
37	311.5	17.2	400	1	US-07-783-602C-3	Sequence 9, Appl1
38	310.5	17.1	400	1	US-07-783-602C-4	Sequence 10, Appl1
39	310.5	17.1	513	2	US-08-406-855A-21	Sequence 21, Appl1
40	310.5	17.1	513	2	US-09-206-893-21	Sequence 21, Appl1
41	310.5	17.1	372	1	US-08-149-093A-6	Sequence 6, Appl1
42	310	17.1	372	1	US-08-149-093A-7	Sequence 7, Appl1
43	309.5	17.1	398	2	US-09-170-531-5	Sequence 5, Appl1
44	309.5	17.1	398	2	US-09-170-531-6	Sequence 6, Appl1
45	308	17.0	348	3	US-08-875-540-13	Sequence 13, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-466-103A-12  
Sequence 12, Application us/08466103A  
Patent No. 5856124  
GENERAL INFORMATION:  
APPLICANT: Reppert, Steven M.  
APPLICANT: Edisawa, Takashi  
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
RECEPTORS AND USES THEREOF  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTED for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,103A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/319,887  
FILING DATE: 07-OCT-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/261,857  
FILING DATE: 17-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00786/250002  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-466-103A-12

Query Match: 100.0% Score: 1815.0 DB ID: 2  
Best Local Similarity: 100.0% Pred. No.: 3.2e+144 Length: 350

Matches 1581 Divergative 0 Mismatches 0 Indels 0 Gaps 0

UY 1 MGNNSALFNASQVPLPCHGAPFMSIALAQLFTITVDILGNIIVLISVYENKRLPN 60  
 1 MGNNSALFNASQVPLPCHGAPFMSIALAQLFTITVDILGNIIVLISVYENKRLPN 60

DB 1 MGNNSALFNASQVPLPCHGAPFMSIALAQLFTITVDILGNIIVLISVYENKRLPN 60  
 1 MGNNSALFNASQVPLPCHGAPFMSIALAQLFTITVDILGNIIVLISVYENKRLPN 60

UY 61 ANNIIVVSLAADIYVAIPYPLVLMSPFNNQWNIIGYHCOVSGFLMGLSVISIFNITG 140  
 61 ANNIIVVSLAADIYVAIPYPLVLMSPFNNQWNIIGYHCOVSGFLMGLSVISIFNITG 140

DB 61 ANNIIVVSLAADIYVAIPYPLVLMSPFNNQWNIIGYHCOVSGFLMGLSVISIFNITG 120  
 61 ANNIIVVSLAADIYVAIPYPLVLMSPFNNQWNIIGYHCOVSGFLMGLSVISIFNITG 120

UY 121 IANRRCYCHSKYKDKLSSKNSLCYVLLIMLTLAVALNPLAGTQYQPPRYSTFA 180  
 121 IANRRCYCHSKYKDKLSSKNSLCYVLLIMLTLAVALNPLAGTQYQPPRYSTFA 180

DB 121 IANRRCYCHSKYKDKLSSKNSLCYVLLIMLTLAVALNPLAGTQYQPPRYSTFA 180  
 121 IANRRCYCHSKYKDKLSSKNSLCYVLLIMLTLAVALNPLAGTQYQPPRYSTFA 180

UY 181 QVSSAVYIAVAVVHILVMILVILHLYLHLLVAVVAVKPKPKPKPKPKPKPKPKPK 240  
 181 QVSSAVYIAVAVVHILVMILVILHLYLHLLVAVVAVKPKPKPKPKPKPKPKPKPK 240

DB 241 FVVFVFAICWAPLNFISGLAVASDPASVPRIPKPLFVASYMAVFNSCLNAILYGLNG 300  
 241 FVVFVFAICWAPLNFISGLAVASDPASVPRIPKPLFVASYMAVFNSCLNAILYGLNG 300

UY 241 FVVFVFAICWAPLNFISGLAVASDPASVPRIPKPLFVASYMAVFNSCLNAILYGLNG 300  
 241 FVVFVFAICWAPLNFISGLAVASDPASVPRIPKPLFVASYMAVFNSCLNAILYGLNG 300

DB 241 FVVFVFAICWAPLNFISGLAVASDPASVPRIPKPLFVASYMAVFNSCLNAILYGLNG 300  
 241 FVVFVFAICWAPLNFISGLAVASDPASVPRIPKPLFVASYMAVFNSCLNAILYGLNG 300

UY 401 NRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRR 450  
 401 NRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRR 450

DB 401 NRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRR 450  
 401 NRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRR 450

RESULT 2  
 US-08-896-465-6  
 Sequence 6, Application US/08896465  
 Patent No. 5949284

GENERAL INFORMATION:  
 APPLICANT: Rothschild, Max F.  
 APPLICANT: Tugale, Christopher K.  
 APPLICANT: Messer, Lori A.  
 APPLICANT: Tan-Ping, Yu  
 TITLE OF INVENTION: GENES AND GENETIC MARKERS FOR IMPROVED  
 TITLE OF INVENTION: REPRODUCTIVE TRAITS IN ANIMALS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: 401 Grand Avenue, Suite 1200  
 CITY: Des Moines  
 STATE: Iowa  
 COUNTRY: USA  
 ZIP: 50309

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patella Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/896,365  
 FILING DATE: 18-JUL-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/022,180  
 FILING DATE: 19-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nibel, Heidi S.  
 PROSTATION NUMBER: 47,710  
 REFERENCE NUMBER: 1874-02141  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 515-288-3667  
 TELEFAX: 515-288-1348  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 453 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 FUNCTION: type: peptide  
 HYDROPHILIC: No

ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 CELL TYPE: Melanocyte  
 CELL LINE: human melanocyte (epidermal)  
 POSITION IN GENOME:  
 MAP POSITION: 14  
 US-08-896-365-6

Query Match 99.4% Score 1803.5 DB 2 Length 353  
 Best Local Similarity 99.2% Pred. No. 2.9e-143  
 Matches 1581 Divergative 0 Mismatches 0 Indels 3 Gaps 1

UY 1 MGNNSALFNASQVPLPCHGAPFMSIALAQLFTITVDILGNIIVLISVYENKRLPN 60  
 1 MGNNSALFNASQVPLPCHGAPFMSIALAQLFTITVDILGNIIVLISVYENKRLPN 60

DB 1 MGNNSALFNASQVPLPCHGAPFMSIALAQLFTITVDILGNIIVLISVYENKRLPN 60  
 1 MGNNSALFNASQVPLPCHGAPFMSIALAQLFTITVDILGNIIVLISVYENKRLPN 60

UY 59 LNNANIVVSLAADIYVAIPYPLVLMSPFNNQWNIIGYHCOVSGFLMGLSVISIFNITG 117  
 59 LNNANIVVSLAADIYVAIPYPLVLMSPFNNQWNIIGYHCOVSGFLMGLSVISIFNITG 117

DB 61 LNNANIVVSLAADIYVAIPYPLVLMSPFNNQWNIIGYHCOVSGFLMGLSVISIFNITG 120  
 61 LNNANIVVSLAADIYVAIPYPLVLMSPFNNQWNIIGYHCOVSGFLMGLSVISIFNITG 120

UY 181 QVSSAVYIAVAVVHILVMILVILHLYLHLLVAVVAVKPKPKPKPKPKPKPKPKPK 240  
 181 QVSSAVYIAVAVVHILVMILVILHLYLHLLVAVVAVKPKPKPKPKPKPKPKPKPK 240

DB 181 QVSSAVYIAVAVVHILVMILVILHLYLHLLVAVVAVKPKPKPKPKPKPKPKPKPK 240  
 181 QVSSAVYIAVAVVHILVMILVILHLYLHLLVAVVAVKPKPKPKPKPKPKPKPKPK 240

UY 236 VMEVVFVFAICWAPLNFISGLAVASDPASVPRIPKPLFVASYMAVFNSCLNAILYGLNG 300  
 236 VMEVVFVFAICWAPLNFISGLAVASDPASVPRIPKPLFVASYMAVFNSCLNAILYGLNG 300

DB 241 FVVFVFAICWAPLNFISGLAVASDPASVPRIPKPLFVASYMAVFNSCLNAILYGLNG 300  
 241 FVVFVFAICWAPLNFISGLAVASDPASVPRIPKPLFVASYMAVFNSCLNAILYGLNG 300

UY 236 LNNANIVVSLAADIYVAIPYPLVLMSPFNNQWNIIGYHCOVSGFLMGLSVISIFNITG 117  
 236 LNNANIVVSLAADIYVAIPYPLVLMSPFNNQWNIIGYHCOVSGFLMGLSVISIFNITG 117

DB 301 NRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRR 353  
 301 NRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRRKRR 353

RESULT 3  
 US-08-896-420-2  
 Sequence 2, Application US/08896420  
 Patent No. 6037131

GENERAL INFORMATION:  
 APPLICANT: Reppert, Steven M.  
 TITLE OF INVENTION: MELANIN 1A RECEPTOR GENE  
 TITLE OF INVENTION: REGULATORY REGIONS AND USES THEREOF  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Fish & Richardson, P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: US  
 ZIP: 02110-2804

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows95  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/896,420  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/896,701  
 FILING DATE:  
 APPLICATION NUMBER: 60/022,185  
 FILING DATE: 18-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Janis K.  
 REGISTRATION NUMBER: 34,819  
 REFERENCE NUMBER: 1874-02142

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-507  
TELEFAX: 617/542-890

TELEX: 200154

INFORMATION FOR SEQ ID NO: 2

SEQUENCE CHARACTERISTICS:

LENGTH: 353 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-09-290-420-2

Query Match 86.5% Score 1570.5 DB 3 Length 253

Best Local Similarity 84.1% Pred. No. 7.9e-124

Matches 297, Conservative 28, Mismatches 25, Indels 3, Gaps 1

1 MGNNGSALPMSQPYL---PGDGRPSWLASALACVLIFFITVDILGNTLVLSYRNKK 57

1 MKGNVSELLNATQAPGGEGGRPRPSMASTLAFITITVDILGNTLVLSYRNKK 60

58 LRNAGNIFVSLAVADLVVAIYPPVLMSTFNNGNLGYLHCQVSGFLMGLSVIGSIFN 117

61 LRNSGNIFVSLAVADLVVAIYPPVLTSLNNGWNLGYLHCQVSAFLMGLSVIGSIFN 120

118 ITGAIINRCYCHSLKDKLYSSKNSLCYVLLTLLTAAVLNLRAGTLYQDPRIYSC 177

121 ITGAIINRCYCHSLKDKLYSSKNSLCYVLLTLLTAAVLNLRAGTLYQDPRIYSC 180

178 TPAQSSASATIAVAVFHFELPMIIVIFCYLRIMLVLYQVQPKPKPKQDPENF 237

181 ITQSSASATIAVAVFHFELPMIIVIFCYLRIMLVLYQVQPKPKPKQDPENF 240

238 VTMEVVFVFLAICAPLNIFGLAVASDPASVPRIPEMLFVASYMAAFNSCLNLIYGL 297

241 VTMEVVFVFLAICAPLNIFGLAVASDPATVPRIPEMLFVASYMAAFNSCLNLIYGL 300

298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

APPLICATION NUMBER: 08/261,857

FILING DATE: 17-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Fraser, Janis K

REGISTRATION NUMBER: 34,819

REFERENCE/AGENT NUMBER: 00786/250002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8905

INFORMATION FOR SEQ ID NO: 14

SEQUENCE CHARACTERISTICS:

LENGTH: 353 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

US-08-466-103A-14

Query Match 85.5% Score 1552.5 DB 2 Length 253

Best Local Similarity 83.3% Pred. No. 2.5e-122

Matches 294, Conservative 28, Mismatches 28, Indels 3, Gaps 1

1 MGNNGSALPMSQPYL---PGDGRPSWLASALACVLIFFITVDILGNTLVLSYRNKK 57

1 MKGNVSELLNATQAPGGEGGRPRPSMASTLAFITITVDILGNTLVLSYRNKK 60

58 LRNAGNIFVSLAVADLVVAIYPPVLMSTFNNGNLGYLHCQVSGFLMGLSVIGSIFN 117

61 LRNSGNIFVSLAVADLVVAIYPPVLTSLNNGWNLGYLHCQVSAFLMGLSVIGSIFN 120

118 ITGAIINRCYCHSLKDKLYSSKNSLCYVLLTLLTAAVLNLRAGTLYQDPRIYSC 177

121 ITGAIINRCYCHSLKDKLYSSKNSLCYVLLTLLTAAVLNLRAGTLYQDPRIYSC 180

178 TPAQSSASATIAVAVFHFELPMIIVIFCYLRIMLVLYQVQPKPKPKQDPENF 237

181 ITQSSASATIAVAVFHFELPMIIVIFCYLRIMLVLYQVQPKPKPKQDPENF 240

238 VTMEVVFVFLAICAPLNIFGLAVASDPASVPRIPEMLFVASYMAAFNSCLNLIYGL 297

241 VTMEVVFVFLAICAPLNIFGLAVASDPATVPRIPEMLFVASYMAAFNSCLNLIYGL 300

298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

Db 298 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 350

301 LQNGPKEYPPIVSLCTARVFFVSSNDVADPVKPKPSPLMTNNVYKDSV 353

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/419,447  
 FILING DATE: 07-OCT-1994  
 PRIOR APPLICATION DATA: 08/419,447  
 FILING DATE: 17-JUN-1994  
 APPLICATION NUMBER: 08/419,447  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FRASER, JAMES K.  
 REGISTRATION NUMBER: 34,419  
 REFERENCE/DOCKET NUMBER: 08/419,447/259002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 366 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MODIFIED TYPE: protein  
 MODIFICATION TYPE: internal  
 US-08-466-103A-4

Query Match 82.98% Score 1505; DR 2; Length 366;  
 Best Local Similarity 81.78; Pred. No. 2,46-118;  
 Matches 287; Conservative 29; Mismatches 33; Indels 4; Gaps 3;

QY 2 QGNG-SALPNASQVFL-EGDGA--FPSWLASALACVLIPTIVDILGNLIVLSVYNNK 57  
 DB 14 KNGSSALLNQSQAAPGAGGVRPPSPMIATIASILIFTIVDIGNLVLSVYNNK 73  
 QY 58 LRNAGNIFVSLAVADLVAVIYPPVLMSTFNNGMNLGHCQVSGFLMGLSVTGSIN 117  
 DB 74 LRNAGNIFVSLAVADLVAVIYPPVLMSTFNNGMNLGHCQVSGFLMGLSVTGSIN 133  
 QY 118 ITGAINRYCYCHSKYDKLYSSKNSLGVLLIMLTILAAVLPNIRAGTIQDPRIYSC 177  
 DB 134 ITGAINRYCYCHSKYDKLYSSKNSLGVLLIMLTILAAVLPNIRAGTIQDPRIYSC 193  
 QY 178 TFAQSSAVTIAVAVHFLVPMIYFCYLRIMILVLOVRQVKKPKQDFRNF 237  
 DB 194 TFAQSSAVTIAVAVHFLVPMIYFCYLRIMILVLOVRQVKKPKQDFRNF 253  
 QY 238 VTMFVVFVFAICAPLNFILGLAVASDPASVPRIPEMLFVASYMAYFNSCLNATLYGL 297  
 DB 254 VTMFVVFVFAICAPLNFILGLAVASDPASVPRIPEMLFVASYMAYFNSCLNATLYGL 313  
 QY 298 LQNGPKYEPPIVSTCTAPVEEVSSNVAQVKKPKPSPMLTNNNVVYDSV 350  
 DB 314 LQNGPKYEPPIVSTCTAPVEEVSSNVAQVKKPKPSPMLTNNNVVYDSV 366

RESULT 6  
 US-08-466-103A-7  
 Sequence 7, Application US/08466365  
 Patent No. 5939264  
 GENERAL INFORMATION:  
 APPLICANT: Rothschild, Max F.  
 APPLICANT: Tugdale, Christopher K.  
 APPLICANT: Mosser, Lori A.  
 TITLE OF INVENTION: GENES AND GENETIC MARKERS FOR IMPROVED  
 TITLE OF INVENTION: REPRODUCTIVE TRAITS IN ANIMALS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENT ADDRESS:  
 ADDRESSEE: Zarley, McKee, Thonle, Voorhees & Sease  
 STREET: 801 Grand Avenue, Suite 400  
 CITY: Des Moines  
 STATE: Iowa  
 COUNTRY: USA  
 ZIP: 50309  
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/466,365  
 FILING DATE: 18-JUL-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/466,365  
 FILING DATE: 18-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nebel, Heidi S.  
 REGISTRATION NUMBER: 37,719  
 REFERENCE/DOCKET NUMBER: TSNR 021591  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 515-288-4667  
 TELEFAX: 515-288-1338  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 366 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: CDNA  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Ovis ammon aries  
 CELL TYPE: Melanocyte  
 US-08-466-365-7

Query Match 82.98% Score 1505; DR 2; Length 366;  
 Best Local Similarity 81.78; Pred. No. 2,46-118;  
 Matches 287; Conservative 29; Mismatches 33; Indels 4; Gaps 3;

QY 2 QGNG-SALPNASQVFL-EGDGA--FPSWLASALACVLIPTIVDILGNLIVLSVYNNK 57  
 DB 14 KNGSSALLNQSQAAPGAGGVRPPSPMIATIASILIFTIVDIGNLVLSVYNNK 73  
 QY 58 LRNAGNIFVSLAVADLVAVIYPPVLMSTFNNGMNLGHCQVSGFLMGLSVTGSIN 117  
 DB 74 LRNAGNIFVSLAVADLVAVIYPPVLMSTFNNGMNLGHCQVSGFLMGLSVTGSIN 133  
 QY 118 ITGAINRYCYCHSKYDKLYSSKNSLGVLLIMLTILAAVLPNIRAGTIQDPRIYSC 177  
 DB 134 ITGAINRYCYCHSKYDKLYSSKNSLGVLLIMLTILAAVLPNIRAGTIQDPRIYSC 193  
 QY 178 TFAQSSAVTIAVAVHFLVPMIYFCYLRIMILVLOVRQVKKPKQDFRNF 237  
 DB 194 TFAQSSAVTIAVAVHFLVPMIYFCYLRIMILVLOVRQVKKPKQDFRNF 253  
 QY 238 VTMFVVFVFAICAPLNFILGLAVASDPASVPRIPEMLFVASYMAYFNSCLNATLYGL 297  
 DB 254 VTMFVVFVFAICAPLNFILGLAVASDPASVPRIPEMLFVASYMAYFNSCLNATLYGL 313  
 QY 298 LQNGPKYEPPIVSTCTAPVEEVSSNVAQVKKPKPSPMLTNNNVVYDSV 350  
 DB 314 LQNGPKYEPPIVSTCTAPVEEVSSNVAQVKKPKPSPMLTNNNVVYDSV 366

RESULT 7  
 US-08-466-103A-6  
 Sequence 6, Application US/08466103A  
 Patent No. 5856124  
 GENERAL INFORMATION:  
 APPLICANT: Reppert, Steven M.  
 APPLICANT: Ebisawa, Takashi  
 TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
 TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENT ADDRESS:

Tue Feb 20 11:42:54 2001

us-09-226-046-12.raii

Page 5

```

ADDRESS: Fish's Richardson P.O.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456.107A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/316,867
FILING DATE: 07-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,857
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/250002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-9906
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal

```

Query Match	79.58	Score 1443.5	DB2	Length 288
Best Local Similarity	96.98	Pred. No. 2.5e-113		
Matches 280; Conservative	1	Mismatches 7		Indels 1
				Gaps 1

```

0Y      62 GNIFVSLAVADLVVAIPIPELVLMSTFNNQWNLGYLHCQVSSGLMSTLVSIGSPNTGI 123
Db      1 GNIFVSLAVADLVVAIPIPELVLMSTFNNQWNLGYLHCQVSSGLMSTLVSIGSPNTGI 60
0Y      122 AINRYCYICHSLKDYCKLXSSKNSLCYVLLIMLLDLAALPVLPRAGTLQYDPRVYSCFFAQ 181
Db      61 AINRYCYICHSLKCKCKLXSSKNSLCYVLLIMLLDLAALPVLPRAGTLQYDPRVYSCFFAQ 119
0Y      182 SVSSAAYTAAVYFHFLLVPMIIVIPFYLPITMLIVQVQPVKPPDPKPKIKPDPFNFIYMF 241
Db      120 SVSSAAYTAAVYFHFLLVPMIIVIPFYLPITMLIVQVQPVKPPDPKPKIKPDPFNFIYMF 179
0Y      242 VYFVFLAIGMAELNIGLAVASDPASXVPIPIEWI FVASYYMAYFNGLNBIIVGLLNQN 301
Db      189 VYFVFLAIGMAELNIGLAVASDPASXVPIPIEWI FVASYYMAYFNGLNBIIVGLLNQN 238
0Y      302 FKREKPRITVSLCTARVFNQSSNDVAPVKKPSPLMTNNNNVAVDSV 350
Db      240 FKREKPRITVSLCTARVFNQSSNDVAPVKKPSPLMTNNNNVAVDSV 288

```

RESULT 8  
 US-08-466-103A-2  
 : Sequence 2, Application US/08466103A  
 : Patent No. 5856124  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Repert, Steven M.  
 : APPLICANT: Ebisawa, Takashi  
 : TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
 : TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
 :  
 : NUMBER OF SEQUENCES: 29

```

CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTECO for Windows Version 2.0.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,103A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/319,887
FILING DATE: 07-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,857
FILING DATE: 17-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/CHECK NUMBER: 3076545002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-03-466-103A-2

```

Query Match	68.5%	Score 1244	DB 2	Length 420
Best Local Similarity	70.4%	Pred. No. 1.6e-96		
Matches 224	Conservative 52	Mismatches 42	Indels 6	Gaps 0

[illegible]

RESTLT 9  
US-08-896-365-8  
; Sequence 8, Application US/08896365  
; Patent No. 5939264  
; GENERAL INFORMATION.





QY 303 KKEENRIVSICARFEVDSNDVADPVMKPS 337  
DB 316 FREYKRILLAMNPRHCTODASKGSHAEOLQSPAP 350

## RESULT 11

US-08-896-365-9  
Sequence 9, Application US/08896365  
Patent No. 5939264  
GENERAL INFORMATION:  
APPLICANT: Rothschild, Max F.  
APPLICANT: Tuggle, Christopher K.  
APPLICANT: Messer, Lori A.  
APPLICANT: Tun-Ping, Yu  
TITLE OF INVENTION: GENES AND GENETIC MARKERS FOR IMPROVED  
TITLE OF INVENTION: REPRODUCTIVE TRAITS IN ANIMALS  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Zarley, McKee, Thome, Voorhees & Sease  
STREET: 801 Grand Avenue, Suite 3200  
CITY: Des Moines  
STATE: Iowa  
COUNTRY: USA  
ZIP: 50309  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/896,365  
FILING DATE: 18-JUL-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/022,180  
FILING DATE: 19-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nebel, Heidi S  
REGISTRATION NUMBER: 37,719  
REFERENCE/DOCKET NUMBER: IS/PF 021591  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 515-288-1338  
TELEFAX: 515-288-3667  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 153 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Sus scrofa  
CELL TYPE: Melanocyte  
US-08-896-365-9

Query Match 38.3% Score 696 DB 2: Length 153:  
Best Local Similarity 34.3% Pctd No 2.8e-51:  
Matches 129: Conservative 11: Mismatches 13: Indels 0: Gaps 0:  
QY 126 YCYCHS:KYDKYSSKNSLCYVLLIM:LTLPVLPPLPAGTLCVPPRYSTTFPAOSVSS 185  
DB 1 YCYCHS:KYDKYSSKNSLCYVLLIM:LTLPVLPPLPAGTLCVPPRYSTTFPAOSVSS 60  
QY 186 AYIAVVFHFLVPIVITYEYITWTIVLCVPPVXPDPRPKLPPDPFNFYTMFVVVY 245  
DB 61 AYIAVVFHFLVPIVITYEYITWTIVLCVPPVXPDPRPKLPPDPFNFYTMFVVVY 120  
QY 246 LFAICMAPLNFILGLAVASDPASMPFRIPFEMLV 278  
DB 121 LFAICMAPLNFILGLAVASDPASMPFRIPFEMLV 153

RESULT 12  
US-08-513-974B-343  
Sequence 343, Application US/0853974B

Patent No. 6114139  
GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohkaki, Tetsuya  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Onogi, Kazuhiro  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
NUMBER OF SEQUENCES: 380  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 15-MAR-1995  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: JP 6-190272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 343:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 349 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-513-974B-443

Query Match 18.6% Score 337.5; DB 3; Length 349;  
 Best Local Similarity 28.2%; Pred. No. 5,5e-21;  
 Matches 93; Conservative 68; Mismatches 124; Indels 45; Gaps 11;

UY 2 QNSGSLPNASQVPLR---GTGAPPSWLSALACVLTIV--VELLSNLVILSVYRNK 56  
 DB 10 KRMNSD-PEPPAPESPPLFGIS-----VENFTLVFGLIFAMGVLSGLVITVLAPSK 62  
 UY 57 --ELPNAGNIEVYSLAVAGLVAVIYPLVLSIENKMLGYLQKQSGFIMLSVYS 114  
 DB 63 PCKPSTINIEFTINSLALAVILPQIPQATVATIPVLCATICKTHYFTVSMILVS 122  
 UY 115 IENITGAINRCYICHSIKYDKLSSKNSLCYLLIMLLIAAVLPNIRAGTIQYDPR 174  
 DB 123 IETLAMSVEYVAVIYHSPSSSLVSPNALLQVCFIMLSIAMSPP-----VAYHQRL 176  
 UY 175 YSCIFASV-----SSAVIIIAVVVPHLVPMILVIEFTYLMIVLQVETPRVED 224  
 DB 177 FHRDSNQTPEWQPMKHLKRAVVTPEVGYLLPILICPYAVV---LNLHFKLK-N 232  
 UY 225 RKPKLKPQDFRNFVTFVVFVFLFAICWADLNFICL-----AAVSDPASKVPIRDEMFLVA 279  
 DB 244 MSKKSASVYVATVAVVAVVVCISMIPIHVVHIWAFPGAFPLTPASPFPRIT-----I 296  
 UY 280 SYMAVFNSGLNAILIGLLNQNFREKRPRI 309  
 DB 287 AHCILAVNSGVNPIYAFISNPBRKAVKOV 416

RESULT: 14  
 US-09-513-974B-46  
 Sequence 46; Application US-09-513-974B  
 Patent No. 6114139  
 GENERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Masaki  
 APPLICANT: Fujii, Ryo  
 APPLICANT: Ohnaka, Tetsuya  
 APPLICANT: Fukusumi, Shoji  
 APPLICANT: Ohai, Kazuhiko  
 TITLE OF INVENTION: A PROTEIN COMPLEX PROTECTS PROTEIN.  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 389  
 \*RESPONDENCE ADDRESS:  
 ADDRESS: DR. J. K. ROBINSON, ROBERTS & JOHNSON, LLP  
 STREET: 140 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.00  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US-09/513,974B  
 FILING DATE: 14-SEP-1995  
 CLASSIFICATION: 516  
 PRIOR APPLICATION DATA:  
 PRIOR APPLICATION NUMBER: PCT/JP95/01594  
 FILING DATE: 10-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-093989

FILING DATE: 19-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-057186  
 FILING DATE: 16-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-007177  
 FILING DATE: 20-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-326611  
 FILING DATE: 28-DEC-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-270017  
 FILING DATE: 02-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236357  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236356  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189274  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 INFORMATION FOR SEQ ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 348 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-513-974B-46

Query Match 18.5% Score 335.5; DB 3; Length 348;  
 Best Local Similarity 28.2%; Pred. No. 8e-21;  
 Matches 93; Conservative 68; Mismatches 124; Indels 45; Gaps 11;

UY 2 QNSGSLPNASQVPLR---GTGAPPSWLSALACVLTIV--VELLSNLVILSVYRNK 56  
 DB 10 KRMNSD-PEPPAPESPPLFGIS-----VENFTLVFGLIFAMGVLSGLVITVLAPSK 62  
 UY 57 --ELPNAGNIEVYSLAVAGLVAVIYPLVLSIENKMLGYLQKQSGFIMLSVYS 114  
 DB 63 PCKPSTINIEFTINSLALAVILPQIPQATVATIPVLCATICKTHYFTVSMILVS 122  
 UY 115 IENITGAINRCYICHSIKYDKLSSKNSLCYLLIMLLIAAVLPNIRAGTIQYDPR 174  
 DB 123 IETLAMSVEYVAVIYHSPSSSLVSPNALLQVCFIMLSIAMSPP-----VAYHQRL 176  
 UY 175 YSCIFASV-----SSAVIIIAVVVPHLVPMILVIEFTYLMIVLQVETPRVED 224  
 DB 177 FHRDSNQTPEWQPMKHLKRAVVTPEVGYLLPILICPYAVV---LNLHFKLK-N 232  
 UY 225 RKPKLKPQDFRNFVTFVVFVFLFAICWADLNFICL-----AAVSDPASKVPIRDEMFLVA 279  
 DB 244 MSKKSASVYVATVAVVAVVVCISMIPIHVVHIWAFPGAFPLTPASPFPRIT-----I 296  
 UY 280 SYMAVFNSGLNAILIGLLNQNFREKRPRI 309  
 DB 287 AHCILAVNSGVNPIYAFISNPBRKAVKOV 316







[illegible]

```

seq_name: qb_pat1:AR026631
seq_documentation block:
DEFINITION   AR026631      1095 bp      DNA
VERSION      AR026631
KEYWORDS     AR026631.1  GI:5937471
SOURCE       unknown.
ORGANISM     unknown.
REFERENCE    1 (bases 1 to 1095)
AUTHORS     Repert, S.M. and Ebisawa, T.
TITLE       DNA encoding high-affinity melanin receptors
JOURNAL     Patent: US 5856124-A 11 05-JAN-1999;
FEATURES     location/qualifiers
             1..1085
BASE COUNT   226 A      233 C      270 G      257 T
ORIGIN
alignment_scores:
              length 1015 00          100000  100000  100000
              Ratio: 5.185
Percent Similarity: 100.000    Percent Identity: 100.000
Alignment block:
US-09-226-946-L x AR026631
Align seq 171 to: AR026631 from: 1 to: 1085
1  MetGlnGlyAsnGlySerAlaLeuProAsnAlaSerGlnProValLeuAr 17
|||||
33  ARCGAAGSDDAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 82
|||||
17  GGLYASGGLYAlArProSerTrpLeuAlaSerAlaLeuAlaGlyVal 34
|||||
83  GGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 132
|||||
34  euilePethIleValAlaAspIleLeuGlyAsnLeuLeuValleu 50
|||||
133  TCATCTTACCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 182
|||||
51  SerValIYrAqAsnLysLysLeuAqAsnAlaGlyAsnIlePheVal 67
|||||
183  TGGGTATATGAGAACAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 232
|||||
67  IsrLeuAlaValAlaAspLeuValAlaAlaLysTrpProTrpProLys 84
|||||
233  GAGGATACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 282
|||||
84  alleMetSerIlePheAsnAsnGlyTrpAsnLeuGlyTrpLeuLys 100
|||||
283  TGGGAGATGAGCAAAATTAATCAAGGGGAGGAGGAGGAGGAGGAGGAGGAG 332
|||||
101  GlnValSerGlyPheLeuMetGlyLysSerValIleGlySerIlePhe 117
|||||
333  CAGGTGAGTGGTGTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 382
|||||
117  nileThGlyAlleAlaIleAsnTrpGlyCysTrpIleCysHisSerLeu 134
|||||
383  TATTAATGATATGATATGATATGATATGATATGATATGATATGATATGAT 432
|||||
134  ySTYrAspLysLeuTrpSerSerLysAsnSerLeuGlyTrpValleu 150
|||||
483  AGTGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482
|||||
151  IleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLeuAlaGlyAla 167
|||||
483  ATATGGGATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 532
|||||
167  FlouGltYrAspProAlaIleLysSerGlyThrPheAlaGlnSerValS 184

```









```

651 ACTCTCTACATGACGCTACACCAACAGACAGAGGTTTCACATTCATC 600
198 ValProMetLeuIleValIlePheCysTyrLeuArgIleTyrIleLeu 214
601 GTGGCTATGATATGTCATCTCTCTGCTACTAAGCATATGGGCTGGCT 650
214 IleGlnValArgGlnArgValLysProAspArgLysProLysLeuLysP 231
651 GCTTCAGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 700
241 ProAspPheArgAsnProValThrMetPheValIlePheValLeuPhe 247
701 GCTACAGACTTCAGAGACTTCTGTCACCATGCTGCTGCTGCTGCTGCT 750
248 AlaIleCysTyrPalaProLeuAsnProIleGlyLeuAlaValAlaSer 264
751 GGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
264 ProValSerMetValProArgIleProGluTyrPheValAlaSer 281
801 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850
281 TyrIleMetAlaTyrPheAsnSerCysLeuAsnAlaIleIleTyrGly 297
851 ACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
298 LeuAsnGlnAsnProValGlyGluTyrArgArgIleIleValSerLeu 314
901 GTCATATGCAATTTCACAAACGATACAAACGATATTCCTGCTGCTG 950
314 ThrAlaArgValIlePheValAspSerSerAsnAspValAlaAspArg 331
951 GCAACATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000
331 GlyTyrPheProSerProLeuMetThrAsnAsnValIleLysVal 347
1001 TTAATATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050
348 AsnSerVal 359
1051 GATCTGCT 1059
seq_name: gb-pat1:AR026642
seq_documentation_block:
LOCUS AR026642 1059 bp DNA
DEFINITION Sequence 13 from patent US 5856124.
VERSION AR026642.1 GI:5947472
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1. (bases 1 to 1052)
AUTHORS Reppert,S.M. and Ebisawa,T.
TITLE DNA encoding high-affinity melatonin receptors
JOURNAL Patent US 5856124-A 13 05-JAN-1999
FEATURES
Source 1..1052
Organization="unknown"
BASE COUNT 262 a 277 c 241 g 282 t
ORIGIN
alignment_scores:
Quality: 1552.50 Length: 353
Ratio: 4.662 Gaps: 1
Percent similarity: 94.444 Percent identity: 83.285
alignment_block:
US-09-226-046-12 x AR026642
Align seq 1/1 for AR026642 from 1 to 1052

```

```

1 MetGlnGlyAsnGlySerAlaLeuProAsnAlaSerGlnProValLeu 16
1 ATGAGCGGAGAAATGTAAGCACTGCTTAAATGCTATGCTGCTGCTGCTG 50
17 ..... ArgGlyAspGlyAlaArgProSerTyrPheValAlaSerAlaLeu 31
51 GCGGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 100
31 LeuGlyValLeuIlePheThrIleValValAspIleProGlyAsnLeu 47
101 GCTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
104 CTTTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
48 ValIleLeuSerValTyrArgAsnLysLysLeuArgAsnAlaGlyAsn 64
151 GTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 200
64 PheValValSerLeuAlaValAlaAspLeuValValAlaIleTyrPro 81
201 ATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 250
81 TyrProLeuValLeuMetSerIlePheAsnAsnGlyTyrPasnLeuGlyTyr 97
251 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
98 LeuHisCysGlnValSerGlyPheCysCysGlyTyrGluSerValIleGly 114
301 GTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 350
114 ThrPheAsnIleThrGlyIleAlaIleAsnArgIleCysTyrIleCysH 131
351 CATATTTAACATGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 400
131 SerLeuLysTyrAspLysLeuTyrSerSerLysAsnSerLeuGlyTyr 147
401 AACAGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450
148 ValLeuLeuIleThrLeuLeuThrLeuAlaValLeuProAsnLeuArg 164
451 GTGTCGCTGATATGATATGATATGATATGATATGATATGATATGAT 500
164 GAlaGlyThrLeuGlnTyrAspProArgIleTyrSerCysThrPheAlaG 181
501 AACGCGAATACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
181 InsSerValSerSerValTyrThrThrAlaValValValPheHisPheLeu 197
551 AATTTTCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
198 ValProMetLeuIleValIlePheCysTyrLeuArgIleTyrIleLeu 214
601 GTCCTATGATATGTCATCTCTCTGCTACTAAGCATATGGGCTGGCT 650
214 IleGlnValArgGlnArgValLysProAspArgLysProLysLeuLysP 231
651 GCTTCAGCTTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 700
241 ProAspPheArgAsnProValThrMetPheValIlePheValLeuPhe 247
701 GCTACAGACTTCAGAGACTTCTGTCACCATGCTGCTGCTGCTGCTGCT 750
248 AlaIleCysTyrPalaProLeuAsnProIleGlyLeuAlaValAlaSer 264
751 GGCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800
264 ProValSerMetValProArgIleProGluTyrPheValAlaSer 281
801 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850
281 TyrIleMetAlaTyrPheAsnSerCysLeuAsnAlaIleIleTyrGly 297
851 ACTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900

```

```

298 LeuAsnGlnAspGluGlySerGlyIleValSerLeu 314
|||||
901 CTGAATCAGAAATTCAGAAAGGATCAAAAGATTTATGTCCTGTCG 950
|||||
314 ThrAlaArgValPhePheValAspSerSerAsnAspValAlaAspArg 321
|||||
951 CACAGCCAGATGTTCTTGTGAGAGTCAAAATGAGAGAGCATAGA 1000
|||||
331 AluYrTrpSerProSerProLeuMetThrAsnAsnValValValVal 347
|||||
1001 TTAAGTGAAGCCCTCTCCCTAATACCAATATTAAGTTCTTCCGCG 1050
|||||
348 AspSerVal 350
|||||
1051 GACTCTGTT 1059

seq_name: qb_prl:AB029932S2
seq_documentation_block:
LOCUS AB029932S2 1250 bp DNA PFI 14-APR-2000
DEFINITION Homo sapiens hmella gene for melatonin 1a receptor, exon 2 and
complete cds.
ACCESSION AB029933
VERSION AB029933.1 G1:6045083
KEYWORDS hmella: melatonin 1a receptor.
SEGMENT 2 of 2
SOURCE Homo sapiens white blood cell DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cladiala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (sites)
Edisawa, T., Kajimura, N., Tachiyama, M., Katoh, M., Sekimoto, M.,
Watanabe, T., Ozeki, Y., Ikeda, M., Jodo, T., Sugishita, M., Iwase, T.,
Kamei, Y., Kim, K., Shibui, K., Kudo, Y., Yamada, N., Toyoshima, R.,
Okawa, M., Takahashi, K. and Yamauchi, I.
Allelic variants of human melatonin 1a receptor: function and
prevalence in subjects with circadian rhythm sleep disorders
Biochem Biophys Res Commun 262 (3), 812-837 (1999)
99400459
2 (bases 1 to 1250)
JOURNAL Edisawa, T.
MEDLINE Submitted (12-JUN-1999) to the DDBJ/EMBL/GenBank databases. Takashi,
AUTHORS Edisawa, T.
TITLES Direct Submission
JOURNAL Submitted (12-JUN-1999) to the DDBJ/EMBL/GenBank databases. Takashi,
Edisawa, T.
Moriyama, Saitama Medical School, Dept. of Psychiatry, 38 Morohongo,
Moriyama-cho, Iruma-gun, Saitama 350-0495, Japan
(E-mail: tedisawa@saitama-med.ac.jp, Tel:81-492-76-1213,
Fax:81-492-76-1622)
FEATURES
source
Location/Qualifiers
1..1250
/organism="Homo sapiens"
/db_xref="taxon:9606"
/feature_type="white blood cell"
join(AB029932,1:861 544,145 1063)
/gene="hmella"
join(AB029932,1:361 544,145 1063)
/gene="hmella"
/codon_start=1
/product="melatonin 1a receptor"
/protein_id="BA083803.1"
/db_xref="GI:6045083"
/translation="MGGNSALPYNASQPYLRGDSAPSLASALACVLTITVEILG
NLIVLSYRNRKILPNAGNIFVYSLAVDLVAIVPYLVISFNNGWNLGYHCOV
SGFLMGLSVGSEFNITGLAINFYVYIGSLKDKLYSKSKSLAYLLIMLITLAVL
PNIRAGTIOYDPRIVSCFTFAOSYSAVITAVVHFLLVMIIVIFCYLIMLITLAVL
ORYKPRKRLKQDFKNTFYVTVFVFAICAPNFTGLIAVSPASMPVRIFEML
FVASYRMAIFNSCLNATITVGLNPNKFRFPPIVSLCTAPVPFVNSNDVADPKKK
PSPLMTNNNVKVDV"
exon
195..1063
/gene="hmella"
/number=2
/product="melatonin 1a receptor"
BASE COUNT 286 a 339 c 306 g 319 t
ORIGIN

```

```

alignment_scores:
Quality: 1512.00 Length: 290
Ratio: 5.214 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 99.655

alignment_block:
us-09-226-046-12 x AB029932S2
Align seq 1/1 to: AB029932S2 from: 1 to: 1250

61 AlaGlyAsnIlePheValValSerLeuAlaValAlaAspLeuValAla 77
|||||
191 TCAGGAACATCTTGTGCTGAGCTTACCGGTGGCAGACCTGGGTGGC 240
|||||
77 AluYrTrpSerProSerProLeuMetSerIlePheAsnAsnIleTyr 94
|||||
241 CATTATCCGTAACCCGTTGCTGCTGATGTCATTTAACAGCGGTGGA 290
|||||
94 snLeuGlyTyrLeuHisCysGlnValSerGlyPheLeuMetGlyLeuSer 110
|||||
291 ACCGGGCTATCTGCACCTGCCAAATCATGATGATGATGATGATGATG 340
|||||
111 ValIleGlySerIlePheAsnIleThrGlyIleAlaIleAsnArgTyrC 127
|||||
341 GCATCGGCTCATATTTACACATCACCGCATCCCATCAACCCCTACTG 390
|||||
127 sThrPheAlaGlnSerValSerSerIleTyrThrIleAlaValValP 194
|||||
391 CTACATGCGCCACAGCTCTCAGAGTACAGACAACTGACAGCAAGAC 440
|||||
144 erLeuGlyTyrValLeuLeuIleThrLeuLeuIleAlaValValLeu 160
|||||
441 CCGCTGCTACCTGCTCTCATATGCTGCTGATGCTGATGCTGATGCTG 490
|||||
161 ProAsnLeuArgAlaGlyThrLeuGlnTyrAspProArgIleTyrSer 177
|||||
491 CCCAACCTGCTGCGAGGAGCTCTCCAGTACGAGACGAGATATATATG 540
|||||
177 sThrPheAlaGlnSerValSerSerIleTyrThrIleAlaValValP 194
|||||
541 CACCTGCGCCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 590
|||||
194 hAspIleLeuValPProMetIleIleValIlePheCysTyrLeuArg 210
|||||
591 TCCACTTCTCTCCCATGATCATGATCATGATCATGATCATGATCATG 640
|||||
211 TrpIleLeuValLeuGlnValArgValValValValValValValVal 227
|||||
641 TGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 690
|||||
227 ocysLeuLysProGlnAspPheArgAspPheValThrMetPheValP 244
|||||
691 CAACAGCAACACACAGGACTTCAGGAAATTTTTCACCATGTTTGCTTT 740
|||||
244 heValLeuPheAlaIleCysTyrPalaProLeuAsnPheIleGlyLeuAla 260
|||||
741 TTGCTCTTTTGGCATTTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCT 790
|||||
261 ValAlaSerAspProAlaSerMetValProArgIleProGlyIlePhe 277
|||||
791 GTGGCCCTGACCCCGCCAGCATGCTGCTGCTGCTGCTGCTGCTGCTG 840
|||||
277 eValAlaSerTyrTyrMetAlaTyrPheAsnSerTyrValAsnAlaIle 294
|||||
841 TGGGCGCATGATACATGCGGATTTTTCACAGGCTGCTGCTGCTGCTG 890
|||||
294 IctyGlyLeuLeuAsnGlnAsnPheArgIleGlyGlyTyrArgValIle 310
|||||
891 TATACGAGCTTACTGAACCAAAATTCAGGAAAGAAACAGAGAGATATA 940
|||||
311 ValSerLeuGlyThrAlaArgValPhePheValAspSerSerAsnAsp 327

```



```

BASE COUNT      41771 3 39817 3 32503 3 43777 3 2100 others
ORIGIN
misc_feature    /note="assembly-fragment"
                32503..32530
                /note="assembly-fragment"
misc_feature    25331..28775
                /note="assembly-fragment"
misc_feature    28876..32715
                /note="assembly-fragment"
misc_feature    32816..38105
                /note="assembly-fragment"
misc_feature    38206..43508
                /note="assembly-fragment"
misc_feature    43609..52803
                /note="assembly-fragment"
misc_feature    52904..60454
                /note="assembly-fragment"
misc_feature    60555..67883
                /note="assembly-fragment"
misc_feature    67984..92739
                /note="assembly-fragment"
misc_feature    92640..105366
                /note="assembly-fragment"
misc_feature    105467..120060
                /note="assembly-fragment"
misc_feature    120161..137506
                /note="assembly-fragment"
misc_feature    137607..149317
                /note="assembly-fragment"
misc_feature    clone_end:17
                vector_slide:right"

```

assignment_scores:	
Quality:	1512.00
Ratio:	5.214
Percent Similarity:	100.000
	Percent Identity:
	99.655
	Length:
	Gaps:
	0

```
alignment_block:
```

CS-09-225-048-12 X AC015601/rev ..  
Align seq 1/1 to reverse of: AC015601 from: 1 to: 149317

```

61  AAGAGYASNTLPEPHVAIVALSERLEUVALAVALAASPLEVALVAL 77
   ..:::..
51360  TCASASAAALATITIGTSISAGCTTATAGTAAATGACAAATTCGTAATGAC 5131111
77  ATLEYTPROTYRPROLEVALLEMETSERILEPHEASNAANGLYTPA 94
   |||||
51310  CATTATCGGTACCGGCTTGGTGTATGATGCAATATTATCAATGGGTGAA 512644
94  snLENGLYTYLLECHISCYGQINVAISERLYPHELOUWETOLYLENCT 110
   |||||
51261  ACCTGGGCAATTGCAATGGCAATCAATGGATTTGATATGGGCGGTGAGC 512111111
111  VALLEGLYSERILEPHEASNLCTHRCYILEALILASNAATGYCY 127
   |||||
51210  GTCAATCGGCTGCATATTACCAATCAACCGCAATCGGCTATCAACGGCTACAG 511633333
127  STYRTLECHSHISSERLLELYSTYRSPLYSEUYSERSELYSASNS 144
   |||||
51160  CTACATCTGTCACATCTTAATATACCAAAATGTACACATGCAAGAAACAT 511111111
144  efLEUCSTYVALLEULEUILETRIPLEULENTHREUAAALALEU 160
   |||||
51110  CCTCTGCTACGTCGCTCTTATATGATGCTTCTACGCTGCAAGGCTGCTG 510633333
161  PROASHLEUAGALAGLYTHREUGINLYRASPPICARGLIETYSERY 177
   |||||
51060  CCGAAACCTCCGCGAAGGCACTGCTGATATAGATTCAGACATCTACCTG 510111111
177  stHPHEALAGINSEVALSERSELYALYRTHREALEVALVALP 194
   |||||

```

51910 CACGCTGGCCGACATCGCCGACAGTGGCCGCTGACGACATGGCTATGAGGTT 50961  
194 hehhsphleuValPrometilleValallehegcsTyrleuArgile 210  
50960 TGCACCTCTCTGCTGCGCAATGATGTACTGATCACTTCCTCTTACGGTAGATA 50911  
211 TrpIleuValleuGlnValArgIleArgValIlyspProAspArgIlysp 227  
50910 TCGATGCTGGGCTCTCGACAGGTATACAGATAGAGTGTAAATTTGATGCTGAAC 50861  
227 OlysiouIlyspProGlnAspPheArgAspPheValThimetPheValValP 244  
50860 CAAATGCAACGACAGACAGATGCAAGAAATTTTGTACGATATTTCGCTT 50811  
244 heValleuPheAlallecystTrpAlaProIleuAspPheIleGlyLeuAla 260  
50810 TGTGCTGTTTGGCTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 50761  
261 ValAlaSerAspProAlaSerMetValProArgIleProGluTrpIleuP 277  
50760 GTGGCGCTTGCACCGCGCGCGAGCATGTGCTGCTGCTGCTGCTGCTGCTGCT 50711  
277 eValAlaSerTyrTrpMetAlaTyrPheAsnSerCysLeuAsnAlaIle 294  
50710 CTGGCGCATGTACTGATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 50661  
294 IeTyrGlyLeuLeuAsnGlnAsnPheArgIlyGlyIlyArgArgIleP 310  
50660 TATACGGGCTACTGCAACGCAAAATTTCAAGAGAGATATAGAGAGATATATA 50611  
311 ValSerLeuCysThrAlaArgValPhePheValAspSerSerAsnAspVa 327  
50610 GCTGTGCTGTGTACAGCCAGAGGTGTTCTTTTGTGACAGCTTAACTACGCT 50561  
327 AlaAspArgValIlyTrpIlyProSerProLeuMetIleAsnAsnAsnV 344  
50560 GCGCGCATATGCTTAAATATAAACCGCTGCTGCTGCTGCTGCTGCTGCTGCT 50511  
344 alValIlyValAspSerVal 350  
50510 TAGTAAAGGTGACTCGCT 50491

seq\_name: qb\_ov:GGU31820

```
seq_documentation_block:
  count: 1000
```

DEFINITION Gallus gallus

VERSION U31820.1 GI:1000103

SOURCE chicken.

Eukaryota; Microsporidia; Archaezoa.

Phasianinae; 1 (bases 1 +  
REFERENCE

AUTHORS  
Reppert, S. M.,  
Kojakowski, T.

TITLE	Abstract
Melatonin receptors: subtypes and functions	Abstract

JOURNAL OF NEUROSCIENCE 15 (5)  
MEDLINE 96073557

REFERENCE	2	(bases)	1
AUTHORS	Reppert, S. M.		

TITLE	Direct Submis
JOURNAL	Submitted (18

Chronobiology  
1226, Boston

FEALOKES	LOC
SOURCE	1.

—qp/

1000

1000

```

4. 1065
/codon_start=1
/product="Mel-1a melatonin receptor"
/feature="db_xref=GI:1000104"
/translat="MANGSEINQTVLPDPAPASPPRPWVSTLAIILPTIVD
LGNLVLIVSVRNKKEKLNAGNIEVSLAIDLVAIPYPLVTSVPHNGMNLGLH
CQISFLMELSVQISLKNITGLAENFVYIASHKREKLYEKNLSLVCGLIVLYI
AIVPLFVSGSLQDPRISCTEASVSASATIAVFPFHLPIAIVYCYLRIMLYI
QVRRVKPDNNPRLKPHDFRNFMTFVYFVAFACAPALNIGLAVADPETIPRP
FMLEVSYYMAVFNQCLNALLYGLINQNFREYKIKYVSCIAKAFQDSSNDADRI
RKRSPFLTNKKYKQVSV"
BASE COUNT      271 a      249 c      234 g      311 t
ORIGIN

alignment_scores:
Quality: 1509.00      Length: 347
Ratio: 4.601      Gaps: 1
Percent similarity: 94.524      Percent identity: 89.403

alignment_block:
us-09-226-046-12 x GCG31820
Align seq 1/1 to: GCG31820 from: 1 to: 1065

4 AsnGlySerAlaLeuProAsnAlaSerGlnProValLeuArgGlyAspC1 20
|||||
28 AACGACACGCTTCTCCGCGCGG...GACCGCGCGCGCGAGCGCTCCGC 71
|||||
20 yAlaAspProSerTrpLeuAlaSerAlaLeuAlaGlyValLeuIlePheT 37
|||||
72 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121
|||||
47 helleValAlaSpIleLeuGlyAsnLeuLeuValIleLeuSerValIyr 53
|||||
122 CACTGATTACAAACACACACACACACACACACACACACACACACACAC 171
|||||
54 ArgAsnLysIleLeuArgAsnAlaGlyAsnIlePheValValSerLeuAl 70
|||||
172 CCGAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 221
|||||
70 AValAlaAspLeuValAlaAlaIleTyProTyProLeuValLeuMetS 87
|||||
222 AATGACAACTTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 271
|||||
87 eLlIlePheAsnAsnGlyTPAsnLeuGlyTYrLeuHisGlySerValSer 103
|||||
272 CCGATTTCACAAATGATGATGATGATGATGATGATGATGATGATGAT 321
|||||
104 GlyPheLeuMetGlyLeuSerValIleGlySerIlePheAsnIleThrG1 120
|||||
422 GATTTGTTATGGGCTTACGTCTCATGTCATGATTTTCAATATTACG5 371
|||||
120 yIleValAlaIleAsnAlaTyTySerIleGlyHisSerLeuLysTYrAspL 137
|||||
472 CATTGCTATCAATGCACTCTATATATGCGCAAGCTGCAATATATGACA 421
|||||
137 ySLIleTySerSerLysAsnSerLeuGlyTYrValLeuLeuIlePheLeu 153
|||||
422 AACTGTATACATGACAAACATTTTGTGTGTGTGTGTGTGTGTGTGTGT 471
|||||
154 LeuThrLeuAlaIleValLeuProAsnLeuAlaGlyAlaIleThrLeuG1 170
|||||
472 CTAAACAGTTGTTGTTATTTGCGCAAGCTGTTGCGATCTGACAGA 521
|||||
170 TrpAspProAlaGlyIleTySerGlyThrPheAlaGlnSerValSerSerAlaT 187
|||||
422 TGACGCGACAGATTATTTCTGTACATTTGACACAGCTGTGTGATTTCCCAT 571
|||||
187 yTThrIleAlaValAlaValPheHisPheLeuValProMetIleLeuAl 203
|||||
572 ATACAAATGCAATGCTGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 621
|||||

204 IlePheCysTYrLeuArgIleTrpIleLeuValLeuGlnIleValArgIleAla 220
|||||
622 ACTATTGTATCTATGASAAATATGATGCTGTTGTTATGATGATGATGATG 671
|||||
220 yAlaIleProAspAlaGlySerProLysLeuGlySerProGlyAspPheArgAsp 237
|||||
672 ACTTAAACCAATATATATATATATATATATATATATATATATATATATAT 721
|||||
237 heValIleMetPheValAlaPheValLeuPheAlaIleGlySTPAlaPro 253
|||||
722 TTGTAAACCATGTTTGTGATTTGTATGCTGTTTGTGCTGTTTGTGCTGCT 771
|||||
254 LeuAsnPheIleGlyLeuAlaValAlaSerAspProAlaSerMetValPr 270
|||||
772 TTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 821
|||||
270 GArgIleProGlnTrpLeuPheValAlaAspTYrTYrMetAlaTYrPheAl 287
|||||
822 TATATATGCAAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 871
|||||
287 snSerCysLeuAsnAlaIleIleLeuGlyLeuLeuAsnGlnAsnPheArg 303
|||||
872 ACAGCTGCTTATATGCTTATATATATATATATATATATATATATATATAT 921
|||||
304 LysGlnTyArgArgIleIleValSerLeuGlyThrAlaArgValPheP 320
|||||
922 AGACATATACAAACAAATTTGTGACATTTTGTACACAAACATTTT 971
|||||
320 eValAspSerSerAspValAlaAspArgValLysTrpLysProSerP 337
|||||
972 CCAGACAGTTGTTATATATATATATATATATATATATATATATATATAT 1021
|||||
337 roleuMetThrAsnAsnAsnValAlaLysValAspSerVal 350
|||||
1022 CACTGATTACAAACACACACACACACACACACACACACACACACACAC 1062
|||||

seq_name: gb|cm:0A014109
seq_documentation_block:
LOCUS      0A014109      1149 bp      mRNA      MAM      01-NOV-1996
DEFINITION      Ovis aries Mel-1a melatonin receptor mRNA, complete cds.
ACCESSION      U14109
VERSION      U14109.1
KEYWORDS      GI:602131
SOURCE      sheep.
ORGANISM      Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eultheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE      1 (bases 1 to 1149)
AUTHORS      Reppert,S.M., Weaver,D.R. and Ebisawa,T.
TITLE      Cloning and characterization of a mammalian melatonin receptor that
MEDIATES reproductive and circadian responses
JOURNAL      Neuron 13 (5), 1177-1185 (1994)
MEDLINE      95033233
REFERENCE      2 (bases 1 to 1149)
AUTHORS      Reppert,S.M.
TITLE      Direct Submission
SUBMITTER      Submitted (23-AUG-1994) Steven M. Reppert, Chronobiology,
Children's Service, Massachusetts General Hospital, 32 Fruit St,
Boston, MA 02114, USA
FEATURES
source
1..1149
location/Qualifiers
1..1149
/organism="Ovis aries"
/db_xref="taxon:9940"
/sex="male and female"
/tissue-type="pars tuberalis (pituitary)"
/dev_stage="adult"
49..1149
/note="high-affinity receptor"
/codon_start=1
/product="Mel-1a melatonin receptor"

```

```

/protein_id="AAH17721.1"
/db_xref="GI:602132"
/translation="MAGRLMGSPGPGKNGSSALLNWSQAPAGADGVRPSPWLA
TLASILLFTIVDIVINILVLSVFNKRLRNKRNFFVSTAVADILVAVYPLALA
SIYNGWSLSLSHGLSGMLGSLVIGSVSTIGLAINVYCCICHSLEIRGLKSTNS
LCGYELMTLTLVAVPNLCVGTLCQYDPRIYSCFPOSSAVTLAVVPHFIVMLV
VVEGLRMLALVQVEMKPKLTKPODEPVTMVEVFLFAICWAPLNFGLV
VASDPMAPRIPEMCLFVASYMAFNSCLNATLYLLNQNFQCEYRKLIYSLCTRM
FFVDSNRHVDRIKRPSPILANHLIKVDSV"

BASE COUNT      226 a      227 c      318 g      278 t
ORIGIN

alignment_scores:
  Quality: 1505.00      Length: 353
  Ratio: 4.533      Gaps: 3
  Percent Similarity: 94.051      Percent Identity: 81.303

alignment_block:
  US-09-226-046-12 x OMU14109

Align seg 1/1 to: OMU14109 from: 1 to: 1149

2 GlnjyAsnGly SerAlaLeuProAsnAlaSerGlnProValLeu... 16
88 AAGGCGCAAGCGGACAGCGCGCTGCTGCAACGCTGCGCAAGCGCGCGG 137
17 ATGGTAAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 137
138 CGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 137
31 LacysValLeuLeuPhePheThrIleValValAspIleLeuGlyAsnLeu 47
188 CCICACATCCATCCTTACCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 237
48 ValIleLeuSerValTyrArcAsnLysLysLeuArgAsnAlaGlyAsnI 64
239 GTSSTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 287
64 ePheValValSerLeuAlaValAlaAspLeuValAlaIleTyrProT 81
288 GTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 337
81 yPProLeuValLeuMetSerIlePheAsnAsnGlyTyrPheAsnGlyTyr 97
338 ACCGCTTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 387
98 LeuHIScysAlaValSerGlyPheLeuMetGlyLeuSerValIleGlySe 114
388 CTGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCTG 437
114 rIlePheAsnIleThrGlyIleAlaIleAsnAsnGlyTyrIleGlySH 131
438 CMLHILMGSLATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
131 ISerLeuLysTyrAspLysLeuTyrSerGlyLysSerLeuCysTyr 147
488 ACAGGCTTAAATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537
148 ValLeuLeuIleTyrLeuLeuThrLeuAlaIleValLeuProAsnLeu 164
538 GTGTTCAGATGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 587
164 GalActylThrLeuGlyTyrAspProArgIleTyrSerCysThrPheLeu 181
589 TGTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 637
181 InseValSerSerAlaTyrThrIleAlaValValPheHisPheLeu 197
638 AGTCGCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 687
198 ValPheMetIleIleValIlePheCysTyrIleAlaIleTyrIleLeu 214

688 GTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 737
214 IleuAlaValArgGlnArgValLysProAspArgLysProLysLeuLysP 231
738 TCTTCAGCTCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787
231 rGlnAspPheArgAsnPheValIleThrLePheValIlePheValLeuPhe 247
788 CCCAGGACTTCAGAGATTTTCTGACCATGTTGTGTGTGTGTGTGTGT 837
248 AlaIleCysTrpAlaProLeuAsnPheIleGlyLeuAlaValAlaSerAs 264
838 GCCATTTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 887
264 pProAlaSerMetValProArgIleProGlnTrpLeuPheValAlaSerT 281
888 CCCGCGCAGCAGTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 937
281 yCtyrMetAlaTyrPheAsnSerCysLeuAsnAlaIleIleTyrGlyLeu 297
938 ACTATATGCGCATATTTCAACAGCTGCTGCTGCTGCTGCTGCTGCTG 987
298 LeuAsnGlnAsnPheArgLysGlnTyrArgArgIleIleValSerLeuCy 314
988 CTGACCCAAATTTTCAGCGCAGAGATACGAAAAATATACGCTCATCTG 1037
314 sThrAlaArgValPhePheValAspSerSerAsnAspValAlaAspArgV 331
1038 TACCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1087
331 allysTrpLysProSerProLeuMetIleAsnAsnAsnValValLysVal 347
1088 TTAAGCGCAACCCCTCTCATTAATAGCCACCAATACCATTAATAAGCTG 1137
348 AspSerVal 350
1138 GACTCGCTT 1146

seq_name: gb_pat1:AK026529

seq_documentation_block: 1149 bp GMA FAT 29-SEP-1999
  LOCUS AK026529
  DEFINITION Sequence 3 from patient US 5856124.
  ACCESSION AR026629
  VERSION AR026629.1 GI:5937469
  KEYWORDS
  SOURCE
  ORGANISM
  UNCLASSIFIED.
  REFERENCE 1 (bases 1 to 1149)
  AUTHORS Peppert,S.M. and Ebisawa,T.
  TITLE DNA encoding high-affinity melatonin receptors
  JOURNAL Patent: US 5856124-A 3 05-JAN-1999;
  FEATURES
    source
      1..1149
      /organism="unknown"
  BASE COUNT      226 a      327 c      318 g      278 t
  ORIGIN

alignment_scores:
  Quality: 1505.00      Length: 353
  Ratio: 4.533      Gaps: 3
  Percent Similarity: 94.051      Percent Identity: 81.303

alignment_block:
  US-09-226-046-12 x AR026629

Align seg 1/1 to: AR026629 from: 1 to: 1149

2 GlnjyAsnGly SerAlaLeuProAsnAlaSerGlnProValLeu... 16
88 AAGGCGCAAGCGGACAGCGCGCTGCTGCAACGCTGCGCAAGCGCGCGG 137

```

```

17  ArgGlyAspGlyAla.....ArgProSerTrpLeuAlaSerAlaLeuA 31
18  CGCGGCGGAGCGCTGGCGCGCGCGCTGGCGCGCGCGCGCGCGCGCG 187
41  ArgValLeuLeuLeuLeuLeuLeuValValAlaSplLeuGlyLeuLeu 47
18  CGCGGCGGAGCGCTGGCGCGCGCGCTGGCGCGCGCGCGCGCGCGCG 237
48  ValLeuLeuSerValTyrArgAsnLysLysLeuArgAsnAlaGlyAsn 64
18  CGCGGCGGAGCGCTGGCGCGCGCGCTGGCGCGCGCGCGCGCGCGCG 287
64  GlnValValSerLeuAlaValAlaAspLeuValValAlaIleTyrPro 81
288  GTTGGGCGGAGCGCTGGCGCGCGCGCTGGCGCGCGCGCGCGCGCGCG 237
81  TyrTrpGlnValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 97
68  ACCGCTGGCGGAGCGCTGGCGCGCGCGCTGGCGCGCGCGCGCGCGCG 187
98  LeuHisGlyGlnValSerGlyPheLeuMetGlyLeuSerValIleGly 114
68  GTTGGGCGGAGCGCTGGCGCGCGCGCTGGCGCGCGCGCGCGCGCGCG 437
114  PhePheAsnIlePheGlyLeuAlaIleAsnArgTyrGlyTyrIleGly 131
48  GCTTTGGGCGGAGCGCTGGCGCGCGCGCTGGCGCGCGCGCGCGCGCG 487
121  IsetLeuLeuTyrAspLysLeuTyrSerSerLysAsnSerLeuGlyTyr 147
488  ACGAGCTGGAGTATGCGTATGCGTATGCGTATGCGTATGCGTATGCG 537
148  ValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 164
68  GCTTTGGGCGGAGCGCTGGCGCGCGCGCTGGCGCGCGCGCGCGCGCG 687
164  GlnAlaGlyPheLeuGlyTyrAspProArgIleTyrSerGlyPheAla 181
68  TGTGGGCGGAGCGCTGGCGCGCGCGCTGGCGCGCGCGCGCGCGCGCG 637
181  InsValValSerSerAlaTyrTrpIleAlaValValPheHisPheLeu 197
68  ACGAGCTGGAGTATGCGTATGCGTATGCGTATGCGTATGCGTATGCG 687
198  ValProMetIleIleValIlePheGlyTyrLeuArgIleTrpIleLeu 214
68  GCTTTGGGCGGAGCGCTGGCGCGCGCGCTGGCGCGCGCGCGCGCGCG 747
214  LeuGlnValValArgGlnArgValLysTrpAspArgLysProGlyLeu 231
748  TGTGGGCGGAGCGCTGGCGCGCGCGCTGGCGCGCGCGCGCGCGCGCG 787
231  GlnAspGlnArgAsnValValValValValValValValValValVal 247
788  GCGAGCTGGAGTATGCGTATGCGTATGCGTATGCGTATGCGTATGCG 847
248  AlaIleGlySerTrpAlaProLeuAsnProIleGlyLeuAlaValAs 264
848  GCGAGCTGGAGTATGCGTATGCGTATGCGTATGCGTATGCGTATGCG 967
264  ProAlaSerMetValProArgIleProGlyTrpLeuPheValAlaSer 291
888  GCGAGCTGGAGTATGCGTATGCGTATGCGTATGCGTATGCGTATGCG 947
291  TyrTrpMetAlaTyrPheAsnSerGlyLeuAsnAlaIleIleTyrGly 297
948  ACGAGCTGGAGTATGCGTATGCGTATGCGTATGCGTATGCGTATGCG 987
298  LeuAsnLeuAsnProArgLysGlyTyrArgArgIleIleValSerGly 314
988  GTTGGGCGGAGCGCTGGCGCGCGCGCTGGCGCGCGCGCGCGCGCGCG 1037

```

```

314  sThralArgValPhePheValAspSerSerAsnAspValAlaAspArg 331
1038  TACGAGCAACAGTCTCTTTTATATATATATATATATATATATATAT 1087
331  aLysTrpLysProSerProLeuMetThrAsnAsnAsnValValLysVal 347
1088  TTAAAGAGTATATATATATATATATATATATATATATATATATATAT 1137
348  AspSerVal 350
1138  GACTGCGGT 1146

seq_name: gb|com:AF045219

seq_documentation_block:
  LOCUS   AF045219      1219 bp      mRNA
  DEFINITION   Ovis aries Mel 1a melatonin receptor mRNA, complete cds.
  ACCESSION   AF045219
  VERSION     AF045219.1 GI:2865610
  KEYWORDS
  SOURCE      Sheep.
  ORGANISM    Ovis aries
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Cetartiodactyla; Fungimantia; Perissodactyla; Bovidae;
              Caprinae; Ovis.
  REFERENCE  1 (bases 1 to 1219)
              Barrett, P., Conway, S., Jockers, R., Strohberg, A.D.,
              Guardiola-Ibanez, A., Delaunay, P., and Morgan, P.J.
              Cloning and functional analysis of a polymorphic variant of the
              Ovis Mel 1a melatonin receptor
              Biochim. Biophys. Acta 1356 (3), 299-307 (1997)
  JOURNAL    MEDLINE
  MEDLINE    9737902
  REFERENCE  2 (bases 1 to 1219)
              Barrett, P., Conway, S. and Morgan, P.J.
              Direct Submission
              Submitted (28-JAN-1998) Mol. Endocrinol. Natl. Biotech. Resour.
              Rd, Aberdeen AB21 9SB, UK
  FEATURES
  source
  1..1219
      /organism="Ovis aries"
      /db_xref="taxon:9940"
      /note="3'-protein coupled receptor; polymorphic variant"
  CDS
      24..1124
      /note="3'-protein coupled receptor; polymorphic variant"
      /product="Mel 1a melatonin receptor"
      /protein_id="AAC6699.1"
      /db_xref="GI:2865611"
      /translation="MAFLWSPGTFPGNSGALLNNSAARAGAGGRRPRSLAA
      TLASLIETIVDIVGNLIVLSVYRNKLRAGVAVSLAVDLIAVPIPLALA
      SLVNNQWSLSSTHGGTSGFMWLSVGEVPSITGAIARVCTCHSLPYCKIYSTNS
      LCVFLIWLITLVAIVPNCVGLQYDPRIVSCITQSSASVIAVVFPIPLMV
      VECVLPITVAIVGVPMVKVPPNKKPKIPQDPNPNVTVVEVFAIOWAPINFGIV
      VASDPSPAPRIPEMLVLEIVASVYMAVFNSCLNATITVILINQNPQVKKIIVSLCTKM
      FIVGSSHRVAPRIVKPTSTIANPVIYVDS"
  BASE COUNT      251 a      337 c      330 g      301 t
  ORIGIN
  alignment_scores:
      quality: 149.00      length: 353
      Ratio: 4.529
  Percent Similarity: 93.768      Percent Identity: 81.303
  alignment_block:
  US-09-226-046-12 x AF045219
  Align seq 1/1 to: AF045219 from: 1 to: 1219
  2 GlnGlyAsnGly.....SerAlaLeuProAsnAlaSerGlnProValLeu... 16
  63 AACGCGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 112
  17 ArgGlyAspGlyAla.....ArgProSerTrpLeuAlaSerAlaLeuA 31

```













[illegible]

	seq_id	document	standard_block:
XX	ID	T09950	Standard Block NA: 1085 BP.
XX	AC	T09950;	
XX	D1	16-AUG-1996	(first entry)
DE	HIGH-affinity melatonin-1A receptor gene.		
KM	Melatonin-1A receptor; human; S protein coupled receptor;		
FW	mellatonin recepteur-animal; Melatonin Receptor-analogs;		
KW	Oxidation reproductive cycle animal breeding puberty;		
KX	antibody transgenic animal drug screening ds.		
OS	Homo sapiens.		
XX	key	longevity/Qualifiers	
FT	CDS	/start=33..1085	
PT	/product=High affinity melatonin-1A receptor		
PX	MO9535320-Al.		
PD	28-Dec-1995.		
PF	07-JUN-1995.	95MN-HS07360.	
PR	06-JUN-1995.	95US-QJ1987-	
PE	17-JUN-1994.	94US-Q261857	
PR	07-OCT-1994.	94US-QJ1987.	
PA	(MASS-) MASSACHUSETTS GEN HOSPITAL.		
XZ	Report SM:		
DR	WP1: 1996-058368/06.		
DP	P-PSEN: P88412.		
XX	RNA encoding high affinity melatonin receptor was used to identify		
PT	receptor agonists or antagonists e.g. for regulating circadian		
PS	rhythm disorders or reproductive cycles		
PS	Claim 8; Fig 5; 11pp; English.		
CC	The sequence encodes full-length human high-affinity melatonin-1A		
OC	receptor, which is a membrane protein, coupled to activate nucleotide		
GC	binding proteins (G-proteins). The gene has been cloned by		
CG	polymerase chain reaction amplification of human genomic DNA, using		
CC	primers derived from the known Lewis melanoma precursor sequence		
CC	(T09947), and use of the product as a probe to obtain clone T09949.		
CC	Screening of a human hypothalamus cDNA library has resulted in		
CC	isolation of the full-length clone. Primers T09950-56 amplify a		
CC	5-kbp band of the gene, and have been used with probe T09942 to		
CC	analyse the tissue distribution of this gene for comparison with the		
CC	melanin-receptor-gene (T09947). Secreted filaments which		
CC	interact with melatonin, or specific antibodies, may be used as		
CC	reporter agents or receptor antagonists. Agonists may be used in		
CC	therapy of circadian rhythm disorders such as jet-lag or day-night		

CC cycle disorders, to control ovulation, or in alteration of  
 CC reproductive cycles in seasonally breeding animals. Antagonists may  
 CC be used to control the initiation or timing of puberty in humans.  
 CC The receptor gene may also be expressed in a transgenic animal for  
 CC use as a model system to screen agonists and antagonists

XX Sequence 1085 BP, 226 A, 323 C, 279 G, 257 T, 0 other.

# alignment\_scores:

Quality: 1815.00 Length: 350  
 Ratio: 5.185 Gaps: 0  
 Percent Similarity: 100.000 Percent Identity: 100.000

# alignment\_block:

us-09-226-046-12 x T09950

Align seq 1/1 to: T09950 from: 1 to: 1085

```

1 MetGlnGlyAsnGlySerAlaLeuProAsnAlaSerGlnProValLeuAr 17
   |||
33 ATGCAAGGAGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 82
   |||
17 GGLYSPGAlaArgProSerTrpLeuAlaSerAlaLeuValLeu 34
   |||
83 CGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 132
   |||
34 euilePheThrIleValAlaAspIleLeuGlyAsnLeuValIleLeu 50
   |||
133 TATCTTACATGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 182
   |||
51 SerValIlyrArgAsnLysLysLeuArgAsnAlaGlyAsnIlePheVal 67
   |||
183 TCGGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 232
   |||
67 IserLeuAlaValAlaAspLeuValAlaIleIlyrProIlyrProLeu 84
   |||
223 GAGCTTACGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 282
   |||
84 alleuMeSerIlePheAsnAsnGlyTrpAsnLeuGlyTyrLeuHisGys 100
   |||
283 TGGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 332
   |||
101 GlnValSerGlyPheLeuMetGlyLeuSerValIleGlySerIlePheAs 117
   |||
333 CAAGTCAAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 382
   |||
117 nileThrGlyIleAlaIleAsnArgTyrCysTyrIleCysHisSerLeu 134
   |||
383 CATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 432
   |||
134 ystyAspLysLeuTyrSerSerLysAsnSerLeuCysTyrValLeuLeu 150
   |||
433 AGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 482
   |||
151 IleTrpLeuLeuThrLeuAlaIleValLeuProAsnLeuArgAlaGlyTh 167
   |||
483 ATATGGTGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 532
   |||
167 LeuGlnIlyrAspTrpArgTrpIleTyrSerCysThrPheAlaGlnSerVal 184
   |||
533 TGTGAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 592
   |||
184 eSerValIlyrThrIleAlaValAlaPheHisPheLeuValProMet 200
   |||
583 GATGAGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 632
   |||
201 IleIleValIlePheCysTyrLeuArgIleTrpIleLeuValLeuGlnVal 217
   |||
633 ATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 282
   |||
217 IATGlnIlyrValIlyrProAspArgIlyrProCysLeuGlyProGlnAsp 234
   |||

```

```

683 CAGACAGACCGTGMACCTGACCGCCAAACCCAACTGAAGAGAGACT 732
234 heuAsnSerPheValIleThrMetProValAlaPheValIlePheAlaIlyCys 750
   |||
733 TACGAAATTTGGACCATGATGATGATGATGATGATGATGATGATGAT 782
   |||
251 TrpAlaProCysAsnSerPheIleGlyLeuAlaValAlaSerAspTrpAlaSer 267
   |||
783 TGGGCTGCTGCTGAGAACTTATGCTGAGAGAGAGAGAGAGAGAGAGAG 832
   |||
267 TrpValIProValGileProGluTrpLeuPheValAlaSerTyrTrpMetAl 284
   |||
833 CATGCTGCTAGATCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 882
   |||
284 IATrPheAsnSerCysLeuAsnAlaIleIleTyrGlyLeuLeuAsnGln 300
   |||
883 CATTATCAACACCTGCTCAAAAGCCATATATACGGCTACCTCAACCA 932
   |||
301 AsnPheArgLysGluTrpArgTrpIleIleValSerLeuCysThrAlaArg 317
   |||
933 AATTCAAGAGAGAGATACAGAGAGATATATAGTCTGCTTGTATACCCAG 982
   |||
317 qValPhePheValAspSerSerAsnAspValAlaAspArgValIlySTPL 334
   |||
983 GGTGTCTTGTGTGACAGAGCTCTTACAGAGAGAGAGAGAGAGAGAGAG 1032
   |||
334 ySProSerProLeuMetThrAsnAsnValValIlyValAspSerVal 350
   |||
1033 AACCGTCTCCACGATGACCAACAAIATATGATGATGATGATGATGAT 1082
   |||
seq_name: /cgn2_2/gcgdata/geneseq/jeneseq/NA1997 NAT-T60593
seq_documentation_block:
ID T60593 standard; CDMN: 1050 BP
XX
XX T60593:
XX
XX 23-JUN-1997 (first entry)
XX
DE Melatonin receptor protein coding sequence.
XX
KW Melatonin receptor protein; human; chinese hamster ovary cell; CHO cell;
KW jet lag; sleeplessness; seasonal melancholia; Alzheimer's disease;
KW dementia; cerebral thrombosis; high blood pressure; cancer; melancholia;
KW ovulation regulator; neurosis; mental confusion; glaucoma; therapy; ds.
XX
OS Homo sapiens.
XX
XX JP09084581-A.
XX
XX 31-MAR-1997.
XX
XX 26-SEP-1995; 95JP-0248177
XX
XX 26-SEP-1995; 95JP-0248177.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX WPI: 1997-252999/23.
XX
XX P-PRO: W15746
XX
XX Facombinant human melatonin receptor protein and (ant)agonists -
XX used for treating jet lag, Alzheimer's disease, melancholia,
XX neurosis, etc.
XX
XX Claim 2: Page 15, 21pp, Japanese.
XX
XX This sequence represents the coding sequence for the human melatonin
XX receptor protein. This sequence is used in an expression vector
XX designated PARKO-hmCIP7. The expression vector is used to produce the
XX chinese hamster ovary (CHO) cells of the invention. The CHO cells express
XX the human melatonin receptor protein and can be used to identify
XX compounds (such as agonists and antagonists) having affinity to the

```













```

198 ATTCAAACTACAGACTTCAGAAATTTGTCACCAATGTTGGTTTG 547
245 aluaphealaiaecystripalaproleusaphealiocyleualaia 261
348 TCGTTTGCCATTGGTGGCTCCCTGTGAACTCAATTCAGCCGGCCG 597
262 AluSerAproAlaserMetValProAilProGluTripleuPheVa 278
598 GCGCTGACCCCGCCAGCATGTCCTGAAATTCGACGCTGCTGTTG 547
278 lAlaserTyrMetAlatyrPheAnsSerCysLeuAlaAlaIle 295
648 GCGCACTATACATGCGCTATTTCACAGCTGCCCATGCCATTAA 697
295 yrcly-leu-eu-asg-l-asn-fhe-as-ly-sci-ty-a-r-a-g-i-le-va-l 311
698 CGGCGTACTGGAACCAAAATTCAGAGAGATACAGAGAAATTATAG 747
312 SerleucysthrAlaIvalPhePheValAspSerSerAsnValAl 328
748 TCCTTGCTGACAGCCAGGTTGTTCTTTGGACAGCTTACAGCTGG 797
328 aAspAvalIystrIlyPheSerProleuMetIhrAsnAsnValV 345
798 CCAIAGAGTTAAATGSAAGCCGTGCTGCTGATGATGATCAATAT 847
345 allysValAspSerVal 350
848 TAAAGGTGAGCTCGTT 864

seq_name: /usr2/seq/seq/seq/seq/VN1907 EXT T79064
seq_documentation_block:
ID T79064 standard; cDNA to mRNA; 1147 bp.
XX
XX 179064:
XX
XX 10-NOV-1997 (first entry)
XX
XX Xenopus melatonin receptor MEL-1Aa short form coding sequence.
XX
XX Allele: Xenopus laevis; melatonin receptor; untranslated region; PCR;
XX mRNA; half-life; skin; amplification; primer; polymerase chain reaction;
XX transmembrane domain; cellular signalling; inhibitor; adenylyl cyclase;
XX modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase; ss.
XX
XX Xenopus laevis.
XX
XX Key Location/Qualifiers
XX CDS 1..1065
XX /tag= a
XX /product= MEL-1Aa receptor protein
XX
XX W09704094-A1.
XX
XX 06-FEB-1997.
XX
XX 24-JUL-1996; 96WO-FR01167.
XX
XX 24-JUL-1995; 95FR-000847
XX
XX (ADIR) ADIR & CIE.
XX
XX Jockers R, Marullo S, Strosberg AD.
XX
XX WPI: 1997-132635/12.
XX
XX F-PSDB: W25976.
XX
XX New nucleic acid encoding functional melatonin receptor of Xenopus
XX for screening for potential (antagonists useful for e.g. treating
XX cardiovascular disease and cancer
XX
XX Claim 1: Page 29-29, 52pp. French.

```

```

XX
XX Sequences 179063-66 represent novel allelic genes of the Xenopus laevis
XX melatonin receptor MEL-1A. The sequences encode proteins which are 65
XX amino acids shorter than those described in the prior art. Also the last
XX 2 C-terminal amino acids encoded by these sequences are different from
XX the previously known proteins. This sequence is a short form of the novel
XX receptor MEL-1Aa also known as Mel 1-(alpha). As compared to the novel
XX form (179063), the difference occurs in the 3' untranslated region (both
XX sequences encode the same protein), which is thought to affect the
XX half-life of the mRNA. The nucleotide sequence was isolated from cDNA
XX derived from Xenopus skin RNA and amplified using the primers 179067-76.
XX The nucleotide sequence encodes a protein which is a 7 transmembrane
XX receptor involved in cellular signalling. MEL-1Aa has been shown to
XX inhibit adenylyl cyclase, but both proteins can modulate intracellular
XX cGMP, esp. inhibiting its accumulation induced by an inhibitor of
XX phosphodiesterase.
XX
XX Sequence 1147 BP; 317 A; 234 C; 242 G; 354 T; 0 other:
XX
XX
XX alignment_scores:
XX      Quality: 1244.00      Length: 318
XX      Ratio: 4.290          Gaps: 0
XX Percent Similarity: 91.195 Percent Identity: 70.440
XX
XX alignment_block:
XX us-09-226-046-12 x T79064
XX
XX Align seg 1/1 to: T79064 from: 1 to: 1147
XX
XX 26 leuAluSerAlaIleAluCyValIleuIlePheIhrIleValValAsp 42
XX 91 CTGACTTGTGCTGACAGCCAGGTTGTTCTTTGGACAGCTTACAGCTGG 140
XX 42 eleuGlyAsnleuValIleleuSerValTyrArgAsnIySylsleuA 59
XX 141 CTTGACCAATATATATGTTCTGTTCTGTTCTGTTCTGTTCTGTTCTG 190
XX 59 rGAsnAlaGlyAsnIlePheValValSerleuAlaValAlaAspVal 75
XX 191 AGAATGCTGAAATGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
XX 76 ValAlaIleTyrProIyProleuValIleuMetSerIlePheAsnSng 92
XX 241 GTTCTGCTGATGCTTATGCTGATGCTTATGCTGATGCTTATGCTGAT 290
XX 92 yTyrAsnleuGlyTyrIleuIleCysIleValIleSerGlyPheleuMet 109
XX 291 GTGACGCTTGGAAATATGATGCTGATGCTGATGCTGATGCTGATGCTG 340
XX 109 euSerValIleGlySerIlePheAsnIleIleGlyIleAlaIleAsn 125
XX 341 TCAGCGTATTCGATTCATGCTGAAATACATACATACATACATACATAC 390
XX 125 TyrCysTyrIleCysHisSerleuTyrAspIySylsCysIySerCys 142
XX 391 TATGCTACATGCTGCGACAGCTGAAATACATACATACATACATACATAC 440
XX 142 SASerleuCystrValleuIleuIleTyrleuIleThrleuAlaVal 159
XX 441 AAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 490
XX 159 aluaphealaiaecystripalaproleusaphealiocyleualaia 175
XX 491 TCGTCCCAAACTTTTGTGTAATCAATATATATATATATATATATATAT 540
XX 176 SerCysThrPheAlaIleSerValSerSerAlaTyrThrIleAlaVal 192
XX 541 TCTGCAATTTGGCGAGAAATGATGCTGCTGCTGCTGCTGCTGCTGCTG 590
XX 192 IValPheHisPheleuValProMetIleIleValIlePheCysIyIle 209
XX 591 GGTGCTATTTATATATATATATATATATATATATATATATATATATAT 640

```





```

|||||
442 TATGATGACATGTCACAAAGGCTGATATGACAAAGCTTATATGCAAAAG 471
142 SASSETLEUcystValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 159
472 AAGGACCTGCTGACCTTGGGCTGACATGATGATGATGATGATGATG 521
159 AAGGACCTGCTGACCTTGGGCTGACATGATGATGATGATGATGATG 175
522 TCGGCTGACATGATGATGATGATGATGATGATGATGATGATGATG 571
176 SerGlyThrPheAlaGlnSerValSerSerAlaTyrThrIleAlaVal 192
572 TCTTGCAATTTGTCACAAAGGCTGCTGATGACCAATGAAAGTAGT 621
192 ValPheHisPheLeuValPheMetIleValIleValIlePheCysTyrLeu 209
622 GGTGCTGACATGATGATGATGATGATGATGATGATGATGATGATG 671
209 TCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 225
672 GAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
226 LysTrpLysLeuLysProGlnAspPheArgAspPheValThrMetPheVal 242
722 AAGCAAAAGCTGACAAACAAACAGACTGACAAATTTCTTGACACATGTT 771
242 ValPheValLeuPheAlaIleCysTyrPalaProLeuAspPheIleLyl 259
772 GGTGCTGACATGATGATGATGATGATGATGATGATGATGATGATG 821
259 GAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 275
822 TCTTGCAATTTGTCACAAAGGCTGCTGATGACCAATGAAAGTAGT 871
276 LeuPheValAlaSerTyrTyrMetAlaTyrPheAsnSerCysLeuAsnAl 292
872 GGTGCTGACATGATGATGATGATGATGATGATGATGATGATGATG 921
292 AlieLleTyrTyrLeuLeuAsnGlnAspPheArgLysGlnTyrArgArg 309
922 TCTTGCAATTTGTCACAAAGGCTGCTGATGACCAATGAAAGTAGT 971
309 LysLeuValSerLeuCysThrAlaArgValPhePheValAspSerSerAsn 325
972 TATGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 1021
426 AspValAlaAspArgValIleTyrPheProSerProLeuMetThrAsn 342
1022 GAGGAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1071
442 DASH 443
|||||
1072 CAAT 1075

```

SeqName: T79063-1000seq/1000seq/NA1297 CAT T79063

seq\_documentation\_block:  
ID T79066 standard: CDNA to mRNA: 1147 BP.

XX T79066  
DT 10-NOV-1997 (first entry)

DE Xenopus melanotin receptor MEL-1Ab short form coding sequence-

XX AlieLle: Xenopus laevis: melanin: receptor: untranslated region: PCR;  
XX mRNA: half-life: skin amplification: primer: polynucleotide chain reaction;  
XX Transmembrane domain: cellular signalling: inhibition: adenylyl cyclase;  
XX a half-life: intracellular: cyclic GMP: inhibitor: phosphodiesterase: seq;  
XX Xenopus laevis:  
XX

Key Location/Qualifiers  
FT CDS 1 1965  
FT FT /\*lag= a  
FT PT /product= melanotin receptor MEL-1Ab  
FN W09704094-A1.

06-FEB-1997  
24-MAY-1997 56MD-FP01167  
24-MAY-1997 95FP-0008947  
PA (ADPR ) ADPR & CTE  
PI Dockers F, Marullo S, Strosberg AD;  
XX WPI: 1997-132635/12.  
XX P-PSDB: W25927.

XX New nucleic acid encoding functional melanotin receptor of Xenopus -  
XX PT for screening for potential (ant)agonists useful for e.g. treating  
XX PT cardiovascular disease and cancer  
XX Claim 1, Page 33-34, 62pp: French.

XX Sequences T79063-66 represent novel allelic genes of the Xenopus laevis  
XX melanotin receptor MEL-1A. The sequences encode proteins which are 65  
XX amino acids shorter than those described in the prior art. This sequence  
XX is a short form of the novel receptor MEL-1Ab also known as  
XX Mel 1-c(beta). As compared to the short form (T79066), the difference  
XX occurs in the 3' untranslated region (both sequences encode the same  
XX protein), which is thought to affect the half-life of the mRNA. The  
XX MEL-1Ab sequences also differ from known MEL-1A receptor sequences by  
XX 6 amino acids. The nucleotide sequence was isolated from cDNA derived  
XX from Xenopus skin RNA and amplified using the primers T79067-75. The  
XX nucleotide sequence encodes a protein which is a 7 transmembrane receptor  
XX involved in cellular signalling. MEL-1Ab has been shown to modulate  
XX intracellular cGMP, esp. inhibiting its accumulation induced by an  
XX inhibitor of phosphodiesterase, but unlike MEL-1Aa (T79063) cannot  
XX inhibit adenylyl cyclase activity.

SO Sequence 1147 BP: 313 A: 246 C: 240 G: 348 T: 0 other:

alignment\_scores:  
Quality: 1240.00 Length: 318  
Ratio: 4.276 Caps: 0  
Percent Similarity: 91.195 Percent Identity: 70.440

alignment\_block:  
US-09-226-046-12 x T79066

Align seg 1/1 to: T79066 from: 1 to: 1147

```

26 TCGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 12
|||||
91 CTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 140
42 CLEUGTASnLeuLeuValIleLeuSerValTyrArgAsnLysTyrLeu 59
|||||
141 CTTGGCAATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 190
59 TGAAGAGTASnLeuLeuValIleLeuSerValTyrArgAsnLysTyrLeu 75
|||||
191 AGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
76 ValAlaIleTyrPheTyrProLeuValIleMetSerIlePheAsnAsnG 92
|||||
241 GTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 290
92 TTPASnLeuGlyTyrLeuHisCysGlnValSerGlyPheLeuMetGlyL 109
|||||

```



291	CTGACGCGCTTAAAAATACCAATTCACATATACAGGCTTCTGGATGCGGAA	344	CTGACGCGCTTAAAAATACCAATTCACATATACAGGCTTCTGGATGCGGAA
109	euserValIleGlySerIlePheAsnIleThrGlyIleAlaIleAsnArg	125	euserValIleGlySerIlePheAsnIleThrGlyIleAlaIleAsnArg
341	TCAAGCTATTGGACATCACTCTTCAACATACACACGCTAGCTATCAACAGG	390	TCAAGCTATTGGACATCACTCTTCAACATACACACGCTAGCTATCAACAGG
126	TTCGCTATTCGCTGShisSerLeuGlySerPheGlyLeuTyrSerSerGly	142	TTCGCTATTCGCTGShisSerLeuGlySerPheGlyLeuTyrSerSerGly
391	TATTGATTACATTGGGACACGCTTGAATATATACAAAGGCTTTTAAATCAAG	440	TATTGATTACATTGGGACACGCTTGAATATATACAAAGGCTTTTAAATCAAG
442	SAsnSerLeuGlyTyrValIleLeuIleIlePheLeuThrIleuAlaIleVal	159	SAsnSerLeuGlyTyrValIleLeuIleIlePheLeuThrIleuAlaIleVal
441	AAGACACCGCTGATTCACTTGGCTTGCATGATGATCACTAATCAATTAATGGCA	490	AAGACACCGCTGATTCACTTGGCTTGCATGATGATCACTAATCAATTAATGGCA
159	alleProAsnLeuArgIleGlyThrLeuGlnTyrValAspProArgIleTyr	175	alleProAsnLeuArgIleGlyThrLeuGlnTyrValAspProArgIleTyr
491	TTTGCGCAAACTTTTGTGTGGATCACTACACTATGACCCCGGGAATTTTG	540	TTTGCGCAAACTTTTGTGTGGATCACTACACTATGACCCCGGGAATTTTG
176	SerGlyThrPheAlaGlnSerValSerSerAlaTyrThrIleAlaVal	192	SerGlyThrPheAlaGlnSerValSerSerAlaTyrThrIleAlaVal
541	TCTTGACATATTGGCGACACCGCTAAGTTCCTATTATACATCAACAGTATG	590	TCTTGACATATTGGCGACACCGCTAAGTTCCTATTATACATCAACAGTATG
192	IValPheHisPheLeuValProMetIleIleValIlePheGlyTyrLeu	209	IValPheHisPheLeuValProMetIleIleValIlePheGlyTyrLeu
591	GCTAGTGCATTTTATAGTCCCTCTTAGTGGTGTGACATTCTCTCTACTTAA	640	GCTAGTGCATTTTATAGTCCCTCTTAGTGGTGTGACATTCTCTCTACTTAA
209	ArgIleTyrIleLeuValLeuGlnValArgGlnArgValIleProAspArg	225	ArgIleTyrIleLeuValLeuGlnValArgGlnArgValIleProAspArg
641	GAATATGGCTTTTATATATCCAAAGTCAAAACAAGATAGAACAAACACTTC	690	GAATATGGCTTTTATATATCCAAAGTCAAAACAAGATAGAACAAACACTTC
226	LysProGlyLeuLysProGlnAspPheArgAsnProValThrMetPheVal	242	LysProGlyLeuLysProGlnAspPheArgAsnProValThrMetPheVal
691	AAGCAAAAGTGGACACCAACAGACTTGAGAAATTTCTTGACCATCTTTGCT	740	AAGCAAAAGTGGACACCAACAGACTTGAGAAATTTCTTGACCATCTTTGCT
242	IValPheValLeuPheValIleGlySerPheAlaProGlnAsnProIleGlyLeu	259	IValPheValLeuPheValIleGlySerPheAlaProGlnAsnProIleGlyLeu
741	GGCTCTTCTACTTTTGGCGGCTTGCTGAGACACCTTGAAATTTTATACGGCG	790	GGCTCTTCTACTTTTGGCGGCTTGCTGAGACACCTTGAAATTTTATACGGCG
259	euserValIleSerAspProAlaSerMetValProArgIleProGluTyr	275	euserValIleSerAspProAlaSerMetValProArgIleProGluTyr
791	TTGCTGTGGCAATTAAAGCTACTACAGCGGAGGACCAAGATTTCCAAAGTGG	840	TTGCTGTGGCAATTAAAGCTACTACAGCGGAGGACCAAGATTTCCAAAGTGG
276	LeuPheValIleSerTyrTyrGlnAlaTyrPheAsnSerGlyLeuAsnAl	292	LeuPheValIleSerTyrTyrGlnAlaTyrPheAsnSerGlyLeuAsnAl
841	TTGCTTGTGTTAAGATATTTCATGAGGCAATTTTAAACAGTGTCTTAATCG	890	TTGCTTGTGTTAAGATATTTCATGAGGCAATTTTAAACAGTGTCTTAATCG
292	AlaGlyTyrGlyLeuLeuAsnGlnAsnPheArgGlySerGlyTyrArgArg	309	AlaGlyTyrGlyLeuLeuAsnGlnAsnPheArgGlySerGlyTyrArgArg
891	TGCTATTCACGCTCTGCTAAATCAAAACTTCCGCAAGGAAATTCAAACGAA	940	TGCTATTCACGCTCTGCTAAATCAAAACTTCCGCAAGGAAATTCAAACGAA
309	IleIleValSerLeuGlyThrAlaArgValPhePheValAspSerSerAsn	325	IleIleValSerLeuGlyThrAlaArgValPhePheValAspSerSerAsn
941	TATTATATCTTTATAGCATTCGAAACAGTGTCTTTCTTACCATATTAGAA	990	TATTATATCTTTATAGCATTCGAAACAGTGTCTTTCTTACCATATTAGAA
326	AspValAlaAspArgValIleTyrIleProSerProLeuMetThrAsnAs	342	AspValAlaAspArgValIleTyrIleProSerProLeuMetThrAsnAs
991	GGAGCAACTGACGAGATGTAAGAAATGAAGGCTTCCGACAGTGTACCAACAA	1044	GGAGCAACTGACGAGATGTAAGAAATGAAGGCTTCCGACAGTGTACCAACAA
342	NAAG 343		
341	CAAT 1044		

```
seq_name: /home/conda/.conda/envs/NA141274/
```

seq\_determination\_b100v.  
ID T79065 standard; cDNA to mRNA; 1312 BP.

XX  
AC T79065:  
XX  
XX 10-NOV-1997 (first entry)  
DT  
XX  
DE Xeropops melaniornis re-evictat MEX:JAL: found from seedling specimens  
XX

```

XX XX Xenopus laevis.
XX OS
XX TH Key Location/Qualifiers
XX FT CDS 1..1065
XX FT /tag= a
XX FT /product= melatonin receptor MEL-1Ab
XX FT
XX PM W09704094-A1
XX PD 06-FEB-1997.
XX PP 24-JUL-1996; 96W0-FP01167.
XX PR 24-JUL-1995; 95FR-0008947.
XX PA (AUIF ) AUIF & CIE
XX PI Jockers R, Marullo S, Strassberg AD;
XX DP WPI, 1997-132635/12.
XX DR P-PADB: W25927.
XX PT New nucleic acid encoding functional melatonin receptor of Xenopus -
XX PT for screening for potential (anti)agonists useful for e.g. treating
XX PT cardiovascular disease and cancer
XX PS Claim 1; Page 30-31; 62pp; French.
XX CC Sequences T79063-66 represent novel allelic genes of the Xenopus laevis
XX CC melatonin receptor MEL-1A. The sequences encode proteins which are 65
XX CC amino acids shorter than those described in the prior art. This sequen
XX CC is a long form of the novel receptor MEL-1Ab also known as Mel-1-(beta
XX CC As compared to the short form (T79066), the difference occurs in the 3'
XX CC untranslated region (both sequences encode the same protein), which is
XX CC thought to affect the half-life of the mRNA. The MEL-1Ab sequences als
XX CC differ from known MEL-1A receptor sequences by 6 amino acids. The
XX CC nucleotide sequence was isolated from cDNA derived from Xenopus skin
XX CC and amplified using the primers T79067-76. The nucleotide sequence
XX CC encodes a protein which is a 7 transmembrane receptor involved in
XX CC cellular signalling. MEL-1Ab has been shown to modulate intracellular
XX CC CGMP, esp. inhibiting its accumulation induced by an inhibitor of
XX CC Phosphodiesterase, but unlike MEL-1Aa (T79063) cannot inhibit adenylyl
XX CC cyclase activity.
XX SO Sequence 1312 BP; 365 A; 271 C; 267 G; 409 T; 0 other;

alignment_scores:
      Quality: 1240.00      Length: 318
      Ratio: 4.276          gaps: 0
Percent Similarity 91.13% Percent Identity: 70.440

Alignment_block:
US-C9-226-046-12 x T79065 ..

Align seq 1/1 to: T79065 from: 1 to: 1312

   26  CCGAGGACATATTCGTCAATTTCCTCCTGGAGSAAACAAGACTGC 142
       |||.....|||.....|.....|.....|.....|.....|
    91  CTACCTCTCCCTGAGCTGAGTTGATTAATTCATATTCCTGCTGAGT 140
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   42  elcugiyasnleuValIleuSeuValIyRaqaNylsyleua 59
       :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
   59  rgsnslagiyasnllephevalseuValserleuaIalaspheuu 75
       |||.....|.....|.....|.....|.....|.....|.....|.....|
   141  CCGGGAACATAATTCGTCAATTTCCTCCTGGAGSAAACAAGACTGC 190
       |||.....|.....|.....|.....|.....|.....|.....|.....|
   191  AGAATGCTGSAATTCCTTGTTTATCATTTGTTATTCCTCATTTGCTT 240

```







Assigned 1/1 to: 007304 from: 1 to: 3083

[illegible]

285 TTTPhleasnSerCysLeuSnAlalleIeIyGlyLeuLeuAsnGlnAs 301  
1663 TCAACAATTCCTCGGTGAACAGCATCATTTATTGSCATTCTTCTGTGAAA 1712  
301 nPeatgLyGlnuTyArgArgile 309  
|||||  
713 TTTCAGTAAGAGCCCTATTAAACAAGTG 1737









17 ..... ArgGlyAspGlyValAlaArgProSerThrIleAlaAspAlaLeuA 31  
 1322 .....  
 1323 .....  
 31 LysGlyValIleuIlePheThrIleValAlaAspIleGluGlyAsnLeuLeu 47  
 1370 .....  
 1370 CCGTATCTCATCTTTACCATCTGCGACATCTGCGACATCTGCGACATCTGCG 1419  
 48 ValIleLeuSerValTyrArgAsnLysLysLeuArgAsnIleGlyAsnIle 64  
 1420 GCGATCGCTGCTGCTTACCGCGAAGAAAGCTTACGACATCTGCGACAT 1469  
 64 ePheValIleSerLeuAlaValAlaAspLeuValAlaIleTyrProt 81  
 1470 ATTCTGCGTGAATTAGCTTCTGCGAAGCTTCTGCTGCTTACCGCTT 1519  
 81 TyrProLeuValLeuMetSerIlePheAsnAsnGlyTyrPheLeuGlyTyr 97  
 1520 ATGCGCTGCTGCTGCTGCTTACCGCTTACCGCTGCTGCTGCTGCTGCTG 1569  
 96 LeuHisGlyGlnValSerGlyPheLeuMetGlyLeuSerValIleGlySer 114  
 1570 GTACATCTGCTGCTGCTGCTTACCGCTTACCGCTGCTGCTGCTGCTGCT 1619  
 114 rIlePheAsnIleThrGlyIleAlaIleAspArgTyrGlyTyrIleGlySH 131  
 1620 GATATTGAAATACGCGGATCTGCTTACCGCTTACCGCTTACCGCTTACCG 1669  
 131 IAspSerLeuLysTyrAspLysIleLysSerSerLysAsnSerLeuGlyTyr 147  
 1670 ACAGCTGACAGCTGACAGCTGACAGCTGACAGCTGACAGCTGACAGCTGAC 1719  
 148 ValLeuLeuIleTyrLeuLeuThrIleLeuAlaValLeuProAsnLeuArg 164  
 1720 GTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1769  
 164 GAlaGlyThrLeuGlnTyrAspProArgIleTyrSerGlyThrPheAlaG 181  
 1770 AACCGGAAACATTCAGTAGCATCCCGGATCTGCTGCTGCTGCTGCTGCTG 1819  
 181 InsertIleSerSerAlaTyrThrIleAlaValAlaIlePheHisPheLeu 197  
 1820 AGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1869  
 198 ValProMetIleIleValIlePheCysTyrLeuArgIleTyrIleLeuVal 214  
 1870 ATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1919  
 214 IleGlnValArgGlnArgValLysProAspArgLysProLysLeuLysP 231  
 1920 GCTTAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1969  
 231 rGlnIleAspPheArgAsnPheValThrMetPheValAlaPheValLeuPhe 247  
 1970 CCGAGGACTTACGAACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2019  
 248 AlaIleCysTrpAlaPheLeuAsnPheIleGlyLeuAlaValAlaSerAs 264  
 2020 GCGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2069  
 264 PheAlaIleSerMetValProArgIleProGlnTyrPhePheValAlaSer 281  
 2070 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2119  
 281 TyrTyrMetAlaTyrPheAsnSerCysLeuAsnAlaIleIleTyrGlyLeu 297  
 2120 ACTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2169  
 298 LeuAsnGlnAsnPheArgLysGlnTyrArgArgIleIleValSerLeuGly 314  
 2170 GTGAACTGAAATTTACAAAGCAATACAAAGCAATACAAAGCAATACAAAG 2219

314 sThrAlaArgValPhePheValAspSerSerAsnAspValAlaAspArgV 331  
 2220 CACAGCCAAATGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2269  
 342 aLysTyrGlyTyrSerProIleSerThrIleAsnAsnAsnValValIleVal 347  
 2270 TTAAATGAAAGCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2319  
 348 AspSerVal 350  
 2320 CAGCTCTGCTT 2328  
 seq\_name: /csp2.6/pldata/2/103/5E\_Comp seq-us-09-466-103A-13  
 seq\_documentation\_block:  
 : Sequence 13, Application US/08466103A  
 : Patent No. 5856124  
 : GENERAL INFORMATION:  
 : APPLICANT: Reppert, Steven M.  
 : APPLICANT: Ebisawa, Takashi  
 : TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
 : TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
 : NUMBER OF SEQUENCES: 29  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Fish & Richardson P.C.  
 : STREET: 225 Franklin Street  
 : CITY: Boston  
 : STATE: MA  
 : COUNTRY: US  
 : ZIP: 02110-2804  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Diskette  
 : COMPUTER: IBM Compatible  
 : OPERATING SYSTEM: Windows95  
 : SOFTWARE: FastSeq for Windows Version 2.0  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/466, 103A  
 : FILING DATE: 06-JUN-1995  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/319,887  
 : FILING DATE: 07-OCT-1994  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: 08/261,857  
 : FILING DATE: 17-JUN-1994  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Fraser, Janis K.  
 : REGISTRATION NUMBER: 34,819  
 : REFERENCE/SEQRT NUMBER: 3,797,450,000  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 617/542-5070  
 : TELEFAX: 617/542-8906  
 : INFORMATION FOR SEQ ID NO. 13:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1063 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: cDNA  
 : FEATURE:  
 : NAME/KEY: Coding Sequence  
 : LOCATION: 1..1059  
 : OTHER INFORMATION:  
 : US-08-466-103A-13

alignment\_scores:                      length:              353  
     quality: 1552.50  
     ratio: 4.002  
 Percent Similarity: 94.334    Percent Identity: 83.286  
 alignment\_block:  
 US-09-226-046-12 x US-09-466-103A-13

Align seq 1/1 to: US-08-466-103A-13 from: 1 to: 1062

```

1 MetGlnGlyAsnGlySerAlaLeuProAsnAlaSerGlnProValLeu... 16
1 ATGAAAGGTAATGTCAGGCAAGCTGCTCAATGCTCAATGCTCAAGG 50
17 .....ATGCTGCTCAATGCTCAATGCTCAATGCTCAATGCTCAAT 31
17 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 100
41 LacysValLeuLeuPheThrIleValAlaSpIleLeuGlyAsnLeu 47
41 GCTTATGCTCAATGCTCAATGCTCAATGCTCAATGCTCAATGCT 150
48 ValIleLeuSerValIlePheAsnIleLeuArgAsnAlaGlyAsn 64
48 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 200
64 GheValValSerLeuAlaValAlaAspLeuValAlaIleTyrPro 81
64 ATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 250
81 YProLeuValIleuMetSerIlePheAsnAsnGlyTyrAsnLeuGly 97
81 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
97 LeuHisGlyGlyValIleGlyPheLeuMetGlyLeuSerValIleGly 114
97 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350
114 PhePheAsnIleIleThrGlyIleValAlaAspArgTyrGlyIleG 131
114 GATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 400
131 AsnSerLeuIleTyrAsnIleGlySerIleGlySerLeuGlyTyr 147
131 ATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 450
147 ValIleLeuLeuIleTyrPheLeuThrIleValAlaValLeuPro 164
147 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 500
164 GAlaGlyThrLeuGlyTyrAspProArgIleTyrSerGlyThrPhe 181
164 AAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
181 IAsnValSerSerAlaTyrThrIleAlaValValIlePheHisPhe 197
181 AGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
197 ValIlePheMetIleIleValIlePheGlyTyrLeuArgIleTyr 214
197 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 650
214 HisGlnValAlaGlnIleValIlePheAspArgIleTyrSerLeu 231
214 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 700
231 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 750
241 PheGlnAspPheAlaAsnPheValIleThrMetPheValAlaPheVal 247
241 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 290
247 AlaIleGlySerPheAlaPheLeuAsnThrIleGlyLeuAlaValAl 264
247 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
264 PProAlaSerMetValIleProArgIlePheIleTyrPheValAla 281
264 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 330
281 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350
281 YTYrMetAlaIleTyrPheAsnSerCysLeuAsnAlaIleIleTyr 297
281 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT

```

```

851 ACUAGCGGCGGACTTCACACAGCGTGGCTCAACGCAATATATACGACTA 900
298 LeuAsnGlnAsnPheArgIleGlyGlyIleTyrArgArgIleIleValSerLeuGly 314
901 GCTGATTCAGAAATTCACAAAGGAAATACAAAAATATATATGCTGCTGCTG 950
314 sThAlaArgValAlaPhePheValAlaSerSerAsnAspValAlaAspArg 331
951 GACAGGTAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000
331 alystrPlyPlyProSerProLeuMetThrAsnAsnAsnValValIleVal 347
1001 TTAATGTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1050
348 AspSerVal 350
1051 GACTGCTCT 1059

seq_name: us-08-466-103A-13
seq_documentation_block:
  : Sequence 3, Application US-08-466-103A
  : Patent No. 5856124
  : GENERAL INFORMATION:
  : APPLICANT: Reppert, Steven M.
  : APPLICANT: Edisawa, Takashi
  : TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
  : TITLE OF INVENTION: FETTERPROS AND USES THEREOF
  : NUMBER OF SEQUENCES: 29
  : CORRESPONDENCE ADDRESS:
  : ADDRESSEE: Fish & Richardson P.C.
  : STREET: 325 Franklin Street
  : CITY: Boston
  : STATE: MA
  : COUNTRY: US
  : ZIP: 02110-2804
  : COMPUTER READABLE FORM:
  : MEDIUM TYPE: Diskette
  : COMPUTER: IBM Compatible
  : OPERATING SYSTEM: Windows95
  : SOFTWARE: FASTSEQ for Windows Version 2.0
  : CURRENT APPLICATION DATA:
  : APPLICATION NUMBER: US-08-466-103A
  : FILING DATE: 06-JUN-1995
  : CLASSIFICATION: 435
  : PPIOP APPLICATION DATA:
  : APPLICATION NUMBER: 08/319,887
  : FILING DATE: 07-OCT-1994
  : PRIOR APPLICATION DATA:
  : APPLICATION NUMBER: 08/261,857
  : FILING DATE: 17-JUN-1994
  : ATTORNEY/AGENT INFORMATION:
  : NAME: Fraser, Janis K.
  : REGISTRATION NUMBER: 34,819
  : REFERENCE ID: 08-466-103A-13
  : TELEPHONE: 617/542-5070
  : TELEFAX: 617/542-8906
  : INFORMATION FOR SEQ ID NO: 3:
  : SEQUENCE CHARACTERISTICS:
  : LENGTH: 1149 base pairs
  : TYPE: nucleic acid
  : STRANDEDNESS: double
  : TOPOLOGY: linear
  : MOLECULE TYPE: DNA (genomic)
  : FEATURE:
  : NAME/KEY: Coding Sequence
  : LOCATION: 49...1146
  : OTHER INFORMATION:
  : US-08-466-103A-3

alignment_scores:

```















```

APPLICANT: Yu, Lei
TITLE OF INVENTION: Mu Op10d Recombinant Compositions and Methods
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-09-889-108
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/305,518
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: INFA005\WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (cDNA)
FEATURE:
NAME/KEY: CDS
LOCATION: 214 1410
US-08-889-108-1

alignment_scores:
Quality: 328.50 Length: 357
Ratio: 1.557 Gaps: 12
Percent Similarity: 59.104 Percent Identity: 25.770

alignment_block:
US-09-226-046-12 X US-08-889-108-1
Align seq 1/1 to: US-08-889-108-1 from: 1 to: 1618

3 GlyAsnGlySerAlaLeuProAsnAlaSerGlnProValLeuArgGlyAs 19
|||||
367 GGGAAAGCAACAGCTGTGAGTCTTAAAGCGGTAACTGCTTTC 405
19 polyAlaAargProSerTrpLeuAlaSerValLeuAlaGlyValLeuLeu 36
|||||
406 ATGGTCACAGCCATTACATCATGAGCCCTCT 436
36 LeuIleLeu ValValAspIleLeuGlyAsnLeuValIleLeu 50
|||||
437 ACTGATCTGTGTGTAGTGGGCTCTTCGAAACTCTCTGTGAT 486
51 SerValTyrArgAsnGlySerLeuArgAsnAlaGlyAsnIlePheVal 67
|||||
487 GTGATTGATGATACACCAAAATGAAAGACTGCTACCTACATCTT 536
67 IserLeuAlaValAlaAspLeuValValAlaIleTyrProTyrProLeu 84
|||||
537 CAACCTGTGCTGTGTAGAT GGTGTAGAGATATACAGGCTTTC 583
84 AluLeuMetIlePheAsnAsnGlyTrpAsnLeuGlyTyrIleuHisGly 100

```

```

584 AGACGTGCACTACCTGATGGGAATATGCGCTTCTGCACTATCTTTCG 633
101 GlnValSerGlyPheLeuMetGlyLeuSerValIleGlySerIlePheAs 117
|||||
634 AAGATCGATGATCAATACATTACTTACAAACATGTTCCACACATATTAC 683
117 IleThrGlyIleAlaIleAsnArgTyrCysTyrIleCysHisSerLeu 134
|||||
684 CCTCGACCATGACGCGTGACCGCTACATGTTGTTGTCACCACTGCA 733
134 ystTyrAspLysLeuTyrSerSerLysAsnSerLeuGlyValLeuLeu 150
|||||
734 AACCCCTGGATTCCGTACCCCGGAAATGCCAAATGTCACCTGCTGC 783
151 IleTrpLeuLeuThrLeuAlaValLeuProAsnLeuArgAlaGlyTh 167
|||||
784 AACTGATCTCTCTCTTCCATCGCTGCTGCTGTATATGTGATGTAAC 833
167 rLeuGlnTyrAspProAargIleTyrSerCysThrPheAlaGlnSerVal 184
|||||
834 CACAAATACAGGCAAGGCTGTCATATGCACTGCAAGTTCACAGC 883
184 eSerAlaTyr ThrIleAlaValValPheHis 195
|||||
196 PheLeuValProMetIleValIlePheCysTyrLeuArgIleProIle 212
|||||
934 TTCATGATCGCATCTCTCATCATCATCTGTGTGTAC 974
212 cLeuValIleGlnValArgGlnArgValLysProAspArgLysProLys 229
|||||
975 GATGATCTTACGACTACAGAGC GTTGGTATGCTATGAGTCCGAAAG 1021
229 eLysProGlnAspPheArgAsnPheValThrMet PheValValPhe 244
|||||
1022 AAGAGCAAGCAATCTGCGGAGATGCAAGATGATGATGATGATG 1071
245 ValLeuPheAlaIleCysTrpAlaProLeuAsnPheIleGlyLeuAla 261
|||||
1072 GCTGTATTATGCTGCTGAGACCCGATGCAATCTACGTCATCTCA 1121
261 AlaSerAspProAlaSerMetValProArgIleProGlu 274
|||||
1122 AGTC GTGATCAGATTCAGAAACCATTTTC 1153
275 TrpLeuPheValAlaSerTyrTyrMetAlaTyrPheAsn 287
|||||
1154 AGACCGTTTCTCTGCGACCTTCTGTATTCT TTGGTTCAGAGAG 1197
288 SerCysLeuAsnAlaIleIleTyrGlyLeuLeuAsnGlnAsnPheArg 304
|||||
1198 AGCTGCTGATCCAGTCTTTCAGCCCTTCTGATGAAACATCTCAAG 1247
304 sGluTyrArgArgIleIleValSerLeuGlyTrpAlaArgValPhePhe 321
|||||
1248 ATGCTTCAGAGATTTCTGTGATCCCA ACGTGTTCATGATGAAAC 1291
321 AlaSerSerAsnAspValAlaAspArgValLysTrpLysProSerPro 337
|||||
1292 AGCAAAATCTGATCTGAGTTCGTCAGAAATATAGGAAATAGCTTTC 1338
338 LeuMetThrAsnAsnAsnVal 344
|||||
1339 ACGCTATATACAGTG 1353
seq_name: /cgn2_6/ptodata/2/lna/6_COMB.seq-us-08-889-108-3
seq_documentation_block:
; Sequence 3, Application US-09889108
; Patent No. 6103492
; GENERAL INFORMATION:

```

```

1 APPLICANT: YU, Del
2 TITLE OF INVENTION: Mutiploid Receptors: Compositions and Methods
3 NUMBER OF SEQUENCES: 17
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: Arnold, White & Durkee
6 STREET: P. O. Box 4444
7 CITY: Houston
8 STATE: TX
9 COUNTRY: USA
10 ZIP: 77210-4444
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Floppy disk
13 COMPUTER: IBM PC Compatible
14 OPERATING SYSTEM: PC-DOS/MS-DOS
15 SOFTWARE: Patent In Release #1.0, Version #1.25
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/989,108
18 FILING DATE:
19 CLASSIFICATION:
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 08/365,518
22 FILING DATE:
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Wilson, Mark R.
25 REGISTRATION NUMBER: 37,259
26 REFERENCE/INVENT NUMBER: INVA/US/WMX
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 512-418-3000
29 TELEFAX: 512-474-7577
30 INFORMATION FOR SEQ. ID NO: 3:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 1618 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36 M-LECIDE TYPE: DNA (cDNA)
37 FEATURE:
38 NAME/KEY: CDS
39 LOCATION: 319..1235
40 OS-OR: acc-108.4
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

```

[illegible]



[illegible]





```
292 YWMeAlaIyPheAsnSerCysLeuAsnAlaIleIleIyGlyLeuLeu 298
      :::::::::: :::::::::: ::::::::::
1104 GGTGGGCTATGCTCACTCTGGCTTCAACCGTTATTTAG  TGGGCG 1150
      :::::::::: :::::::::: ::::::::::
299 AsnGlnAspHeaArgLysGluIyArqArgIleIleValSerLeuCysTh 315
      :::::::::: :::::::::: ::::::::::
1151 AGCCCGGACTTGGAGAGAGAGCTTGGGAGGCTG  CTATGTGG 1191
      :::::::::: ::::::::::
315 rAlaArq 317
      ::::::
1192 CTGCGCG 1198
```





GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein: protein search, using sw model

Run on: February 18, 2001, 13:20:53 Search time 63.26 seconds  
(without alignments)  
375.675 Million cell updates/sec

Title: US-09-226-046-12  
Perfect score: 1915  
Sequence: 1 MGNQSGALPNASQVPLFPGD VKWKPSPMTNNNVKVDVSV 350

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 195891 seqs, 67900655 residues  
Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: 1: PIR66:  
2: PIR1:  
3: PIR2:  
4: PIR3:  
5: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1815	100.0	350	2	138848 Mel-1a melatonin r
2	1505	92.9	420	2	14469 Mel-1c melatonin r
3	1244	68.5	420	2	15166 melatonin receptor
4	1119	61.7	289	2	572554 Mel1b-melatonin re
5	1088	59.9	362	2	138848 melatonin receptor
6	891.5	49.1	613	2	570520 melatonin receptor
7	754	42.1	156	2	184498 melatonin receptor
8	751	41.4	156	2	162107 galanin receptor 1
9	335	18.5	349	2	154336 mu op1oid receptor
10	333.7	18.1	398	2	155517 mu op1oid receptor
11	326.5	18.0	398	2	155504 probable hormone r
12	323.5	17.9	428	2	113739 beta-4C-adrenergic
13	323.5	17.9	428	2	113739 beta-4C-adrenergic
14	324.5	17.9	418	2	602453 beta-3-adrenergic
15	324.5	17.9	418	2	602453 beta-3-adrenergic
16	322.5	17.8	400	2	532804 beta-1-adrenergic
17	322	17.7	394	2	374209 galanin receptor
18	322	17.7	394	2	374209 mu op1oid receptor
19	319	17.6	392	2	564403 mu op1oid receptor
20	319	17.6	400	2	155553 mu op1oid receptor
21	319	17.5	453	2	155553 beta-adrenergic re
22	317	17.5	453	2	115522 hypothetical prote
23	315	17.4	370	1	152315 C protein-coupled
24	313	17.2	322	2	534592 delta op1oid recep
25	312.5	17.2	400	2	155553 beta-3-adrenergic
26	312	17.2	423	2	155553 somatostatin recep
27	311.5	17.1	423	2	155553 delta op1oid recep
28	310.5	17.1	400	2	155553 beta-3-adrenergic
29	310	17.1	380	2	155553 kappa op1oid recep

30	308	17.0	384	2	A45490	neuropeptide Y/pep
31	307	16.9	466	2	S36794	beta-1-adrenergic
32	306.5	16.9	315	2	A40491	alpha-1-adrenergic
33	306	16.2	345	2	S29348	somatostatin recep
34	305.5	16.8	517	2	A45121	alpha-1B adrenergic
35	305	16.8	369	2	D41795	somatostatin recep
36	303.5	16.7	349	2	S12863	G protein-coupled
37	303.5	16.7	382	2	B46133	neuropeptide Y/pep
38	303	16.7	372	2	B48327	somatostatin recep
39	303	16.7	372	2	S27388	delta op1oid recep
40	303	16.6	369	2	A45291	neuropeptide Y rec
41	302	16.6	369	2	S27388	somatostatin recep
42	301.5	16.6	363	2	S27388	somatostatin recep
43	301.5	16.6	369	2	JC2083	somatostatin recep
44	301.5	16.6	384	2	A47249	brain-specific scm
45	301	16.6	359	2	JH0449	hustanin-12 recep

## ALIGNMENTS

RESULT 1  
138848  
Mel-1a melatonin receptor - human  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 29-Apr-2000  
C:Species: Homo sapiens (man)  
A:Accession: 138848  
R:Reprint: S.M.; Weaver, D.R.; Ebisawa, T.  
N:Neuron 13, 1177-1185, 1994  
A:Title: Cloning and characterization of a mammalian melatonin receptor that mediates  
A:Reference number: 138848; M01D:95033233  
A:Accession: 138848  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-350 <RES>  
A:Cross-references: EMBL:014108; NID:9602129; PIDD:AA017720.1; FID:9602130  
C:Superfamily: Vertebrate rhodopsin

Query Match	100.0%	Score 1815	DB 2	Length 350
Best Local Similarity	100.0%	Pred. No. 2	9e-143	
Matches 350	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MGNQSGALPNASQVPLFPGDARPSMTLASALACVLFITVDILGNLILISYRNKRLN	60	
DB	1	MGNQSGALPNASQVPLFPGDARPSMTLASALACVLFITVDILGNLILISYRNKRLN	60	
QY	61	AGNIFVSLAAVDLVVAIYPYELVMSIFNNQWNLGYLHGVSCFLMGSVISSTINITG	120	
DB	61	AGNIFVSLAAVDLVVAIYPYELVMSIFNNQWNLGYLHGVSCFLMGSVISSTINITG	120	
QY	121	IAINPEGYCHSLKDKLYSSKNSLCYLLIWLTLAAVIFRCSAGTQYDPAIYSTFA	180	
DB	121	IAINPEGYCHSLKDKLYSSKNSLCYLLIWLTLAAVIFRCSAGTQYDPAIYSTFA	180	
QY	181	QSSVSYTIAVAVHFLVWLVIFCYLIMLVLVHGVFERRKRLKSTFPNRYTM	240	
DB	181	QSSVSYTIAVAVHFLVWLVIFCYLIMLVLVHGVFERRKRLKSTFPNRYTM	240	
QY	241	FVVFVLPATCMAPLNFGLAVASDPASVPRIPRELEVASYYMAVFNLSLAITIGLNO	300	
DB	241	FVVFVLPATCMAPLNFGLAVASDPASVPRIPRELEVASYYMAVFNLSLAITIGLNO	300	
QY	301	NFKEVPRITVSCTARVFFVDSNDVADRVKWKSPMTNNNVKVDVS	350	
DB	301	NFKEVPRITVSCTARVFFVDSNDVADRVKWKSPMTNNNVKVDVS	350	

RESULT 2  
145469  
Mel-1a melatonin receptor - sheep  
C:Species: Ovis orientalis aries. QY is amon aries (domestic sheep)  
C:Date: 19-Dec-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Mar-2000

Accession: 14449  
 R. Reppert, S.M. Weaver, D.R. Erisawa, T. Neuron 13, 1177-1185, 1994  
 A:Title: Cloning and characterization of a mammalian melatonin receptor that mediates re  
 A:Reference number: 14848; MID:95033233  
 A:Accession: 14449  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-366 (ERP)  
 A:Cross-references: EMBL:U14109; NID:3502131; FID:AA17721.1; FID:9502132  
 C:Superfamily: vertebrate rhodopsin

Query Match 82.9% Score 1505; FR 2; Length 366  
 Best Local Similarity 81.3% Pred. No. 1,56-117;  
 Matches 287; Conservative 29; Mismatches 33; Indels 4; Gaps 3;

UY 2 UGNG-SALPNASQPV--RBDGA--RPSWLASALACVLTIVDILGNLTVSYRNRK 57  
 DB 14 KNGSANTVNSAAGACAGVPPPSWLAATITITIVDILGNLTVSYRNRK 73  
 UY 78 LKNNKIFVVSALVAVLVAIYPPPLMSIFNMGNCYLQVSGFLMGSLVSGIFN 117  
 DB 74 LKNAQVAVVSLAVADLVAVVPPYPLALASIVNMGWSSLHQGLSGFLMGSLVSGIFN 133  
 UY 118 ITTIALNRYVYCHSLKRYKLSKNSLCVLLIMLITLAALPNRACITLQYDPRYSC 177  
 DB 134 ITTIALNRYVYCHSLKRYKLSKNSLCVLLIMLITLAALPNRACITLQYDPRYSC 193  
 UY 178 TCAQSVSSATIAVAVVHFLVPMIIVFCYLRIMLVLRORVRFDPKPKPKPFENF 237  
 DB 194 TTQSSASATIAVAVVHFLVPMIIVFCYLRIMLVLRORVRFDPKPKPKPFENF 253  
 UY 238 VVVFVVFVFAICWAPLNFIGLAVASDPASVPRIPKLVASYIYAFNSCLNATIGL 297  
 DB 254 VVVFVVFVFAICWAPLNFIGLAVASDPASVPRIPKLVASYIYAFNSCLNATIGL 313  
 UY 298 LKNNKIFVVSATIAVAVVHFLVPMIIVFCYLRIMLVLRORVRFDPKPKPKPFENF 357  
 DB 314 LKNNKIFVVSATIAVAVVHFLVPMIIVFCYLRIMLVLRORVRFDPKPKPKPFENF 366

RESULT 3  
 15166  
 Mel-1c receptor subtype - African clawed frog  
 C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 21-Jan-2000  
 C:Accession: 151666  
 R. Reppert, S.M. Weaver, M.R. Reppert, S.M. Proc. Natl. Acad. Sci. U.S.A. 91, 6133-6137, 1994  
 A:Title: Expression cloning of a high-affinity melatonin receptor from Xenopus oocyte me  
 A:Reference number: 151666; MID:9448591  
 A:Accession: 151666  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-420 (ERB)  
 A:Cross-references: EMBL:U14109; NID:3502131; FID:AA17721.1; FID:9502132  
 C:Superfamily: vertebrate rhodopsin

Query Match 59.5% Score 1444; FR 2; Length 420  
 Best Local Similarity 70.4% Pred. No. 7,76-96;  
 Matches 244; Conservative 52; Mismatches 42; Indels 0; Gaps 0;

UY 26 LNSAAGVIFTVVQFNILVHVSYPNKRIPNAGNIFVSLAVADLVAVVPPVIL 85  
 DB 41 LNSAAGVIFTVVQFNILVHVSYPNKRIPNAGNIFVSLAVADLVAVVPPVIL 90  
 UY 146 MSIFNMGNCYLQVSGFLMGSLVSGIFNITJLAINRYVYCHSLKRYKLSKNSL 145  
 DB 91 LKNAQVAVVSLAVADLVAVVPPYPLALASIVNMGWSSLHQGLSGFLMGSLVSGIFN 150  
 UY 146 QVLLIMLITLAALPNRACITLQYDPRYSCFASVSSATIAVAVVHFLVPMIIVF 205

Accession: 14890  
 R. Reppert, S.M. Weaver, D.R. Erisawa, T. Neuron 13, 1177-1185, 1994  
 A:Title: Cloning and characterization of a mammalian melatonin receptor that mediates re  
 A:Reference number: 14848; MID:95033233  
 A:Accession: 14890  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-366 (ERP)  
 A:Cross-references: EMBL:U14109; NID:3502131; FID:AA17721.1; FID:9502132  
 C:Superfamily: vertebrate rhodopsin

Query Match 61.7% Score 1199; FR 2; Length 289  
 Best Local Similarity 69.9% Pred. No. 1,26-85;  
 Matches 202; Conservative 42; Mismatches 45; Indels 0; Gaps 0;

UY 62 GNVVSLAVAVLVAIYPPPLMSIFNMGNCYLQVSGFLMGSLVSGIFNITJLAINRYVYCHSLKRYKLSKNSLCVLLIMLITLAALPNRACITLQYDPRYSC 121  
 DB 14 KNGSANTVNSAAGACAGVPPPSWLAATITITIVDILGNLTVSYRNRK 73  
 UY 142 LKNNKIFVVSATIAVAVVHFLVPMIIVFCYLRIMLVLRORVRFDPKPKPKPFENF 181  
 DB 61 LKNAQVAVVSLAVADLVAVVPPYPLALASIVNMGWSSLHQGLSGFLMGSLVSGIFN 120  
 UY 182 VVVFVVFVFAICWAPLNFIGLAVASDPASVPRIPKLVASYIYAFNSCLNATIGL 241  
 DB 254 VVVFVVFVFAICWAPLNFIGLAVASDPASVPRIPKLVASYIYAFNSCLNATIGL 313  
 UY 242 VVVFVVFVFAICWAPLNFIGLAVASDPASVPRIPKLVASYIYAFNSCLNATIGL 301  
 DB 194 TTQSSASATIAVAVVHFLVPMIIVFCYLRIMLVLRORVRFDPKPKPKPFENF 253  
 UY 301 LKNNKIFVVSATIAVAVVHFLVPMIIVFCYLRIMLVLRORVRFDPKPKPKPFENF 357  
 DB 314 LKNNKIFVVSATIAVAVVHFLVPMIIVFCYLRIMLVLRORVRFDPKPKPKPFENF 366

RESULT 4  
 13890  
 Mel-1c melatonin receptor - human  
 C:Species: Homo sapiens (man)  
 C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 17-Mar-2000  
 C:Accession: 13890

UY 101 CYLHILWILLIIAIVPNEVSGSLQYPRIFSCFAQIVSSSTITIVVHFLVSVIF 210  
 UY 206 CYLHILWILLIIAIVPNEVSGSLQYPRIFSCFAQIVSSSTITIVVHFLVSVIF 265  
 DB 211 CYLHILWILLIIAIVPNEVSGSLQYPRIFSCFAQIVSSSTITIVVHFLVSVIF 270  
 UY 266 ASVAFPIPEWIFVASYMAVFNSCINAIYGLINQNPVKYPPVILSLTARFVDSN 325  
 DB 271 FVAFKIFPEWIFVASYMAVFNSCINAIYGLINQNPVKYPPVILSLTARFVDSN 330  
 UY 326 DVADRVKPKSPPLMTNN 343  
 DB 331 GGTGKSKSPSPPLMTNN 348

Query Match 61.7% Score 1199; FR 2; Length 289  
 Best Local Similarity 69.9% Pred. No. 1,26-85;  
 Matches 202; Conservative 42; Mismatches 45; Indels 0; Gaps 0;

UY 62 GNVVSLAVAVLVAIYPPPLMSIFNMGNCYLQVSGFLMGSLVSGIFNITJLAINRYVYCHSLKRYKLSKNSLCVLLIMLITLAALPNRACITLQYDPRYSC 121  
 DB 14 KNGSANTVNSAAGACAGVPPPSWLAATITITIVDILGNLTVSYRNRK 73  
 UY 142 LKNNKIFVVSATIAVAVVHFLVPMIIVFCYLRIMLVLRORVRFDPKPKPKPFENF 181  
 DB 61 LKNAQVAVVSLAVADLVAVVPPYPLALASIVNMGWSSLHQGLSGFLMGSLVSGIFN 120  
 UY 182 VVVFVVFVFAICWAPLNFIGLAVASDPASVPRIPKLVASYIYAFNSCLNATIGL 241  
 DB 254 VVVFVVFVFAICWAPLNFIGLAVASDPASVPRIPKLVASYIYAFNSCLNATIGL 313  
 UY 242 VVVFVVFVFAICWAPLNFIGLAVASDPASVPRIPKLVASYIYAFNSCLNATIGL 301  
 DB 194 TTQSSASATIAVAVVHFLVPMIIVFCYLRIMLVLRORVRFDPKPKPKPFENF 253  
 UY 301 LKNNKIFVVSATIAVAVVHFLVPMIIVFCYLRIMLVLRORVRFDPKPKPKPFENF 357  
 DB 314 LKNNKIFVVSATIAVAVVHFLVPMIIVFCYLRIMLVLRORVRFDPKPKPKPFENF 366



DB 1 ONIGSHETKIVGIVSNKSLDYVFLMILLILLAMPNLGILVYPPRLYSSTFGSSSSA 60  
 QY 187 YLIAVVFHFLVPMIVIVIFCYLRIMILVQVQVPPKPKPKPKPKPKPKPKPKPKPK 245  
 DB 61 YLIAVVFHFLVPMIVIVIFCYLRIMILVQVQVPPKPKPKPKPKPKPKPKPKPKPK 220  
 QY 247 PACMAFLNFCILVAVSDPASPAPRPPELPLVASY 292  
 DB 121 PALMAFLNFCILVAVSDPASPAPRPPELPLVASY 156

## RESULT 9

Species: Homo sapiens (man)  
 C.Date: 31-May-1996 #seq:2500; revision 3; May-1996 #ext:change 21-22-1996  
 C.Accession: 159336; J05801; G01765; G02528  
 P.Hetero:0/0; P: Antinoff, P.; Lequert, J.; Laburthe, M.; Mayaux, J.  
 Proc Natl Acad Sci U.S.A. 91: 9780-9783, 1994  
 A>Title: Molecular cloning of a functional human galanin receptor.  
 A.Reference number: 159336; MUID:9502404  
 A>Status: preliminary; translated from GR/EMBL/DBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-349 <HAB>  
 A.Cross-references: GR:14330; NID:q55047; PIRN:AA50767.1; PID:q55048  
 R.Chen, Y.; Mestek, A.; Liu, J.; Hurley, J.A.; Yu, L.  
 Mol. Pharmacol. 44: 812-1993  
 A>Title: Molecular cloning and functional expression of a mu-opioid receptor from rat  
 A.Reference number: 157951; MUID:93341493  
 A.Accession: 157951  
 A>Status: preliminary; translated from cB/EMBL/DBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-398 <R2>  
 A.Cross-references: GR:13969; NID:q348250; PIRN:AA41620.1; PID:q348251  
 R.Eppler, C.M.; Hughes, J.D.; Wang, G.R.; Johnson, R.; Corbett, M.; Luthin, D.R.; Chi  
 J. Biol. Chem. 268: 26447-26451, 1993  
 A>Title: Purification and partial amino acid sequence of a mu-opioid receptor from ra  
 A.Reference number: A46880; MUID:94075333  
 A.Accession: A46880  
 A>Status: preliminary  
 A.Molecule type: protein  
 A.Experimental source: brain membranes  
 A.Note: Sequence extracted from NCBI backboun (NCBI:140841)  
 R.Schiff, M.; Soy, S.; Parakkishan, S.; Digne, P.; Loh, H.H.  
 Biochem Biophys Res Commun. 209: 563-574, 1995  
 A>Title: Cloning and characterization of a mu-opioid receptor from rat postnatal macroph  
 A.Reference number: 152314; MUID:95251654  
 A.Accession: 152314  
 A>Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-340 <SE>  
 A.Cross-references: GR:877843; NID:q3992546  
 R.Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Tateshima, H.  
 FEBS Lett. 327: 331-334, 1993  
 A>Title: Primary structures and expression of cDNA of rat mu-opioid receptor: beta-a  
 A.Reference number: S34592; MUID:93351652  
 A.Accession: S34592  
 A.Molecule type: mRNA  
 A.Residues: 1-344; V: 246-399 <FW>  
 A.Cross-references: GR:10345; NID:q341850; PIRN:AA40652.1; PID:q341857  
 R.Wang, T.  
 Proc Natl Acad Sci U.S.A. 90, 10230-10234, 1993  
 A>Title: Mu opiate receptor cDNA cloning and expression.  
 A.Reference number: A48799; MUID:94052137  
 A.Accession: A48799  
 A>Status: preliminary; translated from GR/EMBL/DBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-244; V: 246-398 <MAN>  
 A.Cross-references: GR:120684; NID:q409449; PIRN:AA41543.1; PID:q409449  
 R.Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J.  
 Neuron 11: 903-913, 1993  
 A>Title: Cloning and pharmacological characterization of a rat mu opiod receptor.

Query Match 18.5% Score 335; DR 2; Length 149;  
 Best local similarity 29.2% Freq. NO. 166-20;  
 Matches 95; Consistency 57; X-matches 129; Indels 21; Gaps 11;

QY 2 OGNISA-LTNASQP-VLPDGAAPPWLASALCVLFTIV-VDLIGMLVLSYPRK- 56  
 DB 10 EGVASFETFAPEPDLFFPS-----VENVTVVPSIFPMASVLSGSLITVYAPSKP 63  
 QY 57 -KRNAGNIPVNSLAVAVI VAVIYPIVLMSTPNNKNGEGLHGVSGFLMGSLVGTST 115  
 DB 64 GKPRSTNPIINLSTADLAFLFCIPGATVYALPTWLGAFICKFTIHYFTVSMVSI 123  
 QY 116 ENITGIAIRYICGLSLYPRKLYSKNSIC/VVILIMITIAAVDPNIPAGTIDYPPY 175  
 DB 124 FTAASVIRVAVIVSRSSSPVSSNALDVGCIWALSTIASPVAIHQGL-FHPAS 182  
 QY 176 SFTFACV SVATIAVVFHFLVPMIVIVIFCYLRIMILVQVQVPPKPKPKPKPKPK 220  
 DB 184 NQTFCKLQWVDFYHKKAVAVVTFVDFYLRILILDFGVAKV---LNHKKKKK-NMSKKS 238

QY 250 KQVLFNIVMEVVFALFALMAPLNFGI-----AASDPASVPIPEMLVASTYMA 284  
 DB 239 EASKKKATVIVVWVGISMI PPHITIRHMAEGVPIIPASTPFI-----TARGLA 292  
 QY 285 YENSCINAIYGLNQNPPPEPPI 309  
 DB 293 YENSCNITIVAFSENPRFAYQV 317

## RESULT 10

mu opiod receptor - rat  
 156517  
 Species: Rattus norvegicus (Norway rat)  
 C.Date: 26-Jul-1996 #sequence:1; revision 4; 26-Jul-1996 #ext:change 20-21-1996  
 C.Accession: 156517; 157951; A46880; 152314; S34592; A48799; 158154  
 R.Burgoyne, J.R.; Zhang, S.; Burrows, C.; Saito, T.; Finkbeiner, S.R.; Peitz, M.; Gran  
 J. Neurochem. 64: 14-24, 1995  
 A>Title: Characterization and distribution of a cloned rat mu-opioid receptor.  
 A.Reference number: 156517; MUID:95094825  
 A.Accession: 156517  
 A>Status: preliminary; translated from GR/EMBL/DBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-398 <R2>  
 A.Cross-references: EMBL:U02083; NID:q403573; PIRN:AA47094.1; PID:q403574  
 R.Chen, Y.; Mestek, A.; Liu, J.; Hurley, J.A.; Yu, L.  
 Mol. Pharmacol. 44: 812-1993  
 A>Title: Molecular cloning and functional expression of a mu-opioid receptor from rat  
 A.Reference number: 157951; MUID:93341493  
 A.Accession: 157951  
 A>Status: preliminary; translated from cB/EMBL/DBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-398 <R2>  
 A.Cross-references: GR:13969; NID:q348250; PIRN:AA41620.1; PID:q348251  
 R.Eppler, C.M.; Hughes, J.D.; Wang, G.R.; Johnson, R.; Corbett, M.; Luthin, D.R.; Chi  
 J. Biol. Chem. 268: 26447-26451, 1993  
 A>Title: Purification and partial amino acid sequence of a mu-opioid receptor from ra  
 A.Reference number: A46880; MUID:94075333  
 A.Accession: A46880  
 A>Status: preliminary  
 A.Molecule type: protein  
 A.Experimental source: brain membranes  
 A.Note: Sequence extracted from NCBI backboun (NCBI:140841)  
 R.Schiff, M.; Soy, S.; Parakkishan, S.; Digne, P.; Loh, H.H.  
 Biochem Biophys Res Commun. 209: 563-574, 1995  
 A>Title: Cloning and characterization of a mu-opioid receptor from rat postnatal macroph  
 A.Reference number: 152314; MUID:95251654  
 A.Accession: 152314  
 A>Status: preliminary  
 A.Molecule type: mRNA  
 A.Residues: 1-340 <SE>  
 A.Cross-references: GR:877843; NID:q3992546  
 R.Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Tateshima, H.  
 FEBS Lett. 327: 331-334, 1993  
 A>Title: Primary structures and expression of cDNA of rat mu-opioid receptor: beta-a  
 A.Reference number: S34592; MUID:93351652  
 A.Accession: S34592  
 A.Molecule type: mRNA  
 A.Residues: 1-344; V: 246-399 <FW>  
 A.Cross-references: GR:10345; NID:q341850; PIRN:AA40652.1; PID:q341857  
 R.Wang, T.  
 Proc Natl Acad Sci U.S.A. 90, 10230-10234, 1993  
 A>Title: Mu opiate receptor cDNA cloning and expression.  
 A.Reference number: A48799; MUID:94052137  
 A.Accession: A48799  
 A>Status: preliminary; translated from GR/EMBL/DBJ  
 A.Molecule type: mRNA  
 A.Residues: 1-244; V: 246-398 <MAN>  
 A.Cross-references: GR:120684; NID:q409449; PIRN:AA41543.1; PID:q409449  
 R.Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J.  
 Neuron 11: 903-913, 1993  
 A>Title: Cloning and pharmacological characterization of a rat mu opiod receptor.

A:Reference number: 158154; MUID:94059560  
 A:Accession: 158154  
 A:Status: preliminary; translated from GR/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-244; V: 246-398 <TR>  
 A:Cross-references: JN:22455; NID:347671; PIRN:AA16075.1; PIR:437672  
 C:Genetics:  
 A:Gene: MUCB1  
 C:Superfamily: vertebrate rhodopsin  
 C:Keywords: 3 protein-coupled receptor; transmembrane protein

Query Match 18.1%; Score 328.5; DB 2; Length 398;  
 Best Local Similarity 25.9%; Pred. No. 6.2e-20;  
 Matches 92; Conservative 76; Mismatches 148; Indels 39; Gaps 12;

3 GAGSALPNASQVPLRGDGRPSWLSALACVLFPI--VVDILNLVLIVSVENKRLRN 60  
 52 GNDSDLPQIGSPS-----MTAITIMALYSIVCGVGFGLVAVYVATKMK 101  
 61 AGNIFVSLAVADLVVAIYPLVLSIFNNGMNGYHCOVSGFLKLSVIGSIENITG 120  
 102 ATNIFYFNALAD-ALATSTLFPQSVNLMGTWPGTICKIVISIDYNNFTSIFLCT 160  
 121 IANRCYCIHSLKIKYKLSKNSLCYVLLIWLTLAAVLPLNLAGTLQYDPRISCTFA 180  
 161 MSVDRIAGCHPVKALDFRPRAKIVNCGMILSALGLPVNEMAITIKYRGSIDCTLI 220  
 181 QVSASV-----TIAVVFHFLVPMIIVFVLFVILVQVQKVKCDFRKLKTCQCF 235  
 221 FSHPTWEMELKIVFIFAFIPILITVY---GLMLRLKS-VRMISGSKEDPNIP 276  
 236 NFVTM-FVAVFVFAICMAPLNFGLVAVSDPASMPRIPEWLF-VASY---MAVENSQ 289  
 277 RIRRMVLVAVVAVIVCIPPIHIVIKK-----LITRETFQVSMHFCALGYNSQ 330  
 290 LNAIIVGLNINFEKVPRIIVSCVAPVFEVSSNDVADPKMKPSPLMTNNV 344  
 331 LNPVLVAFDENKRCRFECP--TSSTIEQNSITFVQNTPEHPS--TANTV 380

RESULT 11  
 mu oploid receptor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #ext\_change 24-Nov-1999  
 C:Accession: 156504  
 R:Zastany, R.L., George, S.P., Nguyen, T., Cheng, R., Tsatsos, J., Briones-Urbina, R.,  
 A:Title: Cloning, characterization, and distribution of a mu-opioid receptor in rat brain  
 A:Reference number: 156504; MUID:94246380  
 A:Accession: 156504  
 A:Status: preliminary; translated from GR/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-398 <PS>  
 A:Cross-references: EMBL:U03424; NID:31017731; PIRN:AA479180.1; PIR:41017732  
 C:Superfamily: vertebrate rhodopsin

Query Match 18.0%; Score 326.5; DB 2; Length 398;  
 Best Local Similarity 25.9%; Pred. No. 9e-20;  
 Matches 92; Conservative 76; Mismatches 148; Indels 39; Gaps 12;

3 GAGSALPNASQVPLRGDGRPSWLSALACVLFPI--VVDILNLVLIVSVENKRLRN 50  
 52 GNDSDLPQIGSPS-----MTAITIMALYSIVCGVGFGLVAVYVATKMK 101  
 61 AGNIFVSLAVADLVVAIYPLVLSIFNNGMNGYHCOVSGFLKLSVIGSIENITG 120  
 102 ATNIFYFNALAD-ALATSTLFPQSVNLMGTWPGTICKIVISIDYNNFTSIFLCT 160  
 121 IANRCYCIHSLKIKYKLSKNSLCYVLLIWLTLAAVLPLNLAGTLQYDPRISCTFA 180

Db 161 MSVDRIAGCHPVKALDFRPRAKIVNCGMILSALGLPVNEMAITIKYRGSIDCTLI 220  
 QY 181 QVSASV-----TIAVVFHFLVPMIIVFVLFVILVQVQKVKCDFRKLKTCQCF 235  
 Db 221 FSHPTWEMELKIVFIFAFIPILITVY---GLMLRLKS-VRMISGSKEDPNIP 276  
 QY 236 NFVTM-FVAVFVFAICMAPLNFGLVAVSDPASMPRIPEWLF-VASY---MAVENSQ 289  
 Db 277 RIRRMVLVAVVAVIVCIPPIHIVIKK-----LITRETFQVSMHFCALGYNSQ 330  
 QY 290 LNAIIVGLNINFEKVPRIIVSCVAPVFEVSSNDVADPKMKPSPLMTNNV 344  
 Db 331 LNPVLVAFDENKRCRFECP--TSSTIEQNSITFVQNTPEHPS--TANTV 380

RESULT 12  
 113739  
 probable hormone receptor 225.13 (similarity) - fruit fly (Drosophila melanogaster)  
 C:Species: Drosophila melanogaster  
 C:Date: 13-Aug-1999 #sequence\_revision 12-Aug-1999 #ext\_change 09-Jun-2000  
 C:Accession: 113739  
 R:Murphy, L.; Harris, D.; Barrell, B.  
 A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.  
 A:Reference number: 217668  
 A:Accession: 113739  
 A:Status: preliminary; translated from GR/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-670 <MP>  
 A:Cross-references: EMBL:AL031765; NID:6337223; PIRN:CAA21123.1  
 C:Genetics:  
 A:Introns: 30/2; 77/2; 400/1  
 A:Note: EG:22E5.11

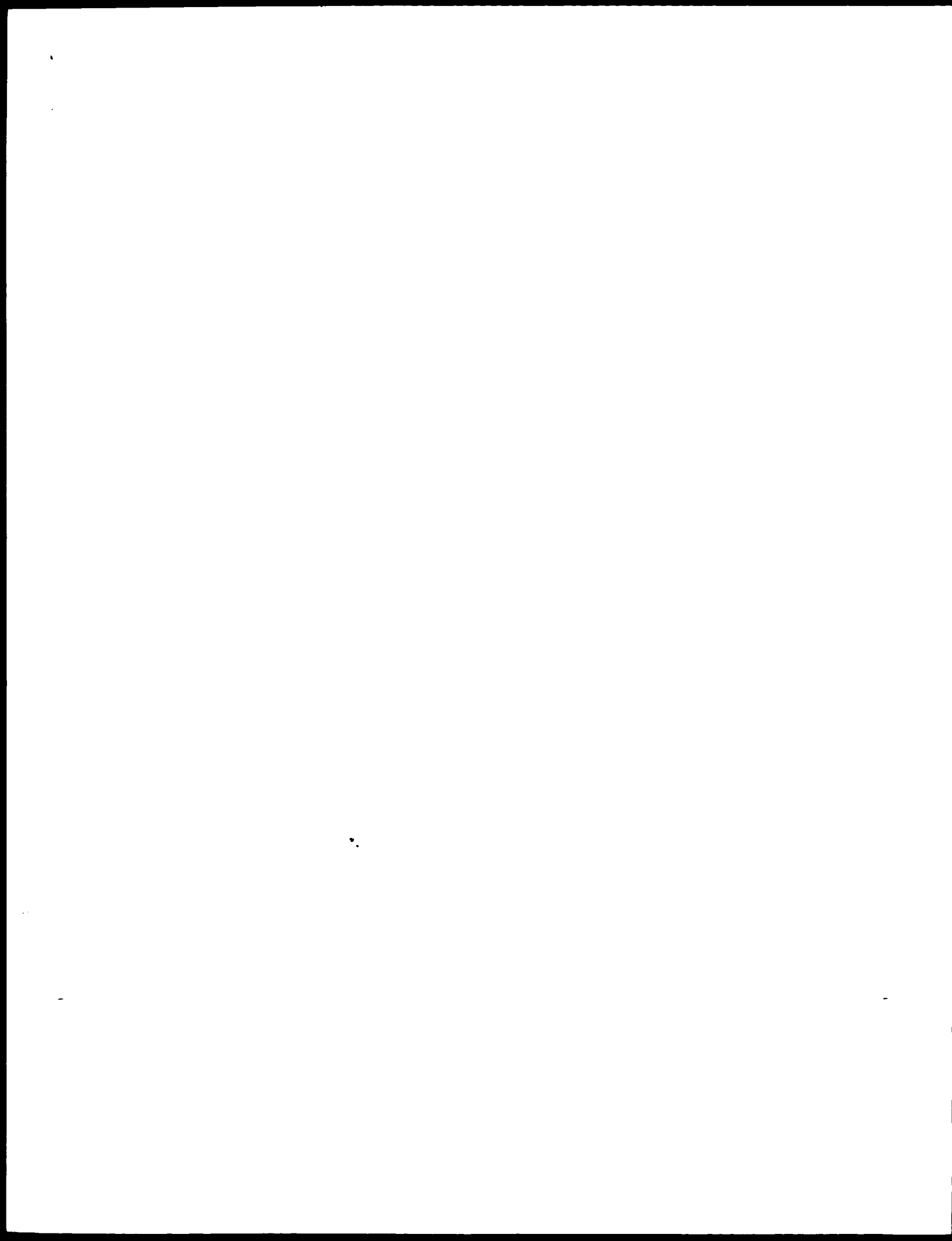
Query Match 17.9%; Score 325.5; DB 2; Length 670;  
 Best Local Similarity 23.8%; Pred. No. 1.8e-19;  
 Matches 92; Conservative 69; Mismatches 139; Indels 87; Gaps 11;

31 ACVLFPI--VVDILNLVLIVSVENKRLRN--FFVSLAVADLVVAIYPLVLSIF 89  
 Db 39 AAVTFLIMIVGICGLNLIVALLKCPKRVNAAAFIISLCIADLLFCALVLPQGERFV 98  
 QY 90 NNGMNGYHCOVSGFLKLSVIGSIFNITGIANRCYCIHSLKIKYKLSKNSLCYVL 149  
 Db 99 QGTWPHQGVCRILPFIQVNGISLCLAMITINRYWITIHGLYARIKYKRWAVMIA 158  
 QY 150 LNLTLAAVLPLNLAG--GTLQYDPRISQ---TPQVSASVTLAVVVFHFLVPMIIV 204  
 Db 159 ACM-FSTQKCLPILGFWPGFVDSPLQSTMTDGHGSKTILFIDA--FVIPCIVII 216  
 QY 205 FGYLPIMILVQVRO----- 219  
 Db 217 ACVAKIIVVYIKSPQSLKPIATYQNSIPNNPLPLNLSGALPNAFQPSNRVSSDSS 276  
 QY 220 -----PVKPDKPKLKPQDFRNFVYFVVFLEFALCQADPLNIGLAV 261  
 Db 277 SHSLVETASGKQCFTPKQGEVAVKPNPITKMYLAHLSVVCYLDPIITVKA- 335  
 QY 262 ASDPASVPRIPKLVFVASYIMATFNSCLNATYGLLNCNFEKVPRIIVSC TARVF 320  
 Db 336 --DKNVEHFS-----LHLCSTILNLSACINELIIVIKKQVPAVATV--TPQPARILL 387  
 QY 321 ----VDSSNDVADPKMKPSPLMTNN 343  
 Db 388 PGKTINGASSAAE---KKKIDLSNNHS 412

RESULT 13  
 A55044  
 beta-4C-adrenergic receptor - turkey  
 C:Species: Melagris gallopavo (common turkey)  
 C:Date: 18-Nov-1994 #sequence\_revision 18-Nov-1994 #ext\_change 13-Aug-1999









GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 18 2001 14:35:34 Search time 54.38 Seconds  
(without alignments)  
207 851 Million cell updates/sec

Title: US-09-226-046-12  
Perfect score: 1815  
Sequence: 1 MGNKSGALPMSQPLRGN3 .....VKKRSPMTNNNVKVDV 350

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 88757 seqs, 32294092 residues  
Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_39.\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	1815	100.0	350 1	MLIA_HUMAN P48039 homo sapien
2	1590.5	87.6	353 1	MLIA_PIG P49317 Phodopus su
3	1570.5	86.5	353 1	MLIA_MOUSE O61184 mus musculu
4	1509	83.1	353 1	MLIA_CHICK P49385 gallus gall
5	1505	82.9	353 1	MLIA_SHEEP P49340 ovis arie
6	1244.5	58.5	420 1	MLIA_CHICK P49219 xenopus lae
7	1234	54.5	420 1	MLIA_XENLA P49219 xenopus lae
8	1175	64.7	257 1	MLIA_BOVIN P502765 bos taurus
9	1119	61.7	257 1	MLIA_CHICK P51050 gallus gall
10	1084	59.9	362 1	MLIA_HUMAN P49385 homo sapien
11	891.5	49.1	613 1	MLIX_SHEEP O13585 homo sapien
12	867.5	47.8	575 1	MLIX_SHEEP O13585 homo sapien
13	862.5	47.5	583 1	MLIX_SHEEP O13585 homo sapien
14	751	41.4	156 1	MLIA_MOUSE O68445 mus musculu
15	700	38.6	154 1	MLIA_PIG O02781 sus scrofa
16	646	35.6	153 1	MLIA_PIG P51046 brachydanio
17	598.5	33.0	152 1	MLIA_PIG P51047 brachydanio
18	592	31.0	152 1	MLIA_XENLA P51047 brachydanio
19	555	30.6	151 1	MLIA_PIG P51047 brachydanio
20	554	30.1	151 1	MLIA_PIG P51047 brachydanio
21	546	29.9	150 1	MLIA_XENLA P51047 brachydanio
22	487.5	26.9	120 1	MLIA_PIG P49287 ratu
23	380	18.7	346 1	GALR_PAT O62305 ratu
24	340	18.7	346 1	GALR_PAT O62305 ratu
25	335.5	18.5	346 1	GALR_PAT O62305 ratu
26	335	18.5	346 1	GALR_PAT O62305 ratu
27	329.5	18.1	346 1	GALR_PAT O62305 ratu
28	326	18.0	401 1	OPRM_BOVIN P49385 gallus gall
29	325	17.9	401 1	OPRM_BOVIN P49385 gallus gall
30	324.5	17.9	401 1	OPRM_BOVIN P49385 gallus gall
31	324.5	17.9	401 1	OPRM_BOVIN P49385 gallus gall
32	322.5	17.7	401 1	OPRM_BOVIN P49385 gallus gall
33	322	17.7	401 1	OPRM_BOVIN P49385 gallus gall

RESULT ID	MLIA_HUMAN	STANDARD	PRT	350 AA.	ALIGNMENTS
34	319	17.6	400 1	OPRM_HUMAN	P35372 homo sapien
35	319	17.6	400 1	OPRM_HUMAN	P07700 melaleucis q
36	317	17.5	352 1	OPRM_HUMAN	P49693 homo sapien
37	317	17.5	352 1	OPRM_HUMAN	P49693 homo sapien
38	315	17.4	455 1	OPRM_HUMAN	P49693 homo sapien
39	315	17.4	455 1	OPRM_HUMAN	P49693 homo sapien
40	315	17.4	455 1	OPRM_HUMAN	P49693 homo sapien
41	315	17.4	455 1	OPRM_HUMAN	P49693 homo sapien
42	312	17.2	455 1	OPRM_HUMAN	P49693 homo sapien
43	312	17.2	455 1	OPRM_HUMAN	P49693 homo sapien
44	312	17.2	455 1	OPRM_HUMAN	P49693 homo sapien
45	311.5	17.2	423 1	OPRM_MOUSE	P30731 mus musculu

RESULT 1  
MLIA\_HUMAN  
ID MLIA\_HUMAN STANDARD PRT 350 AA.  
AC P48039;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE MELANOTIN RECEPTOR TYPE 1A (MEL-1A-R).  
GN MTNRIA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hemo.  
RN [1]  
RP SEQUENCE FROM N.A. AND VARIANTS TRP-54 AND VAL-157.  
RX MEDLINE=95033233; PubMed=7946354;  
PA Peppert S.M., Weaver D.R., Ebisawa T.;  
RT Cloning and characterization of a mammalian melatonin receptor that  
RT mediates reproductive and circadian responses.\*;  
RL Neuron 13:1177-1185(1994).  
RN [2]  
RP SEQUENCE FROM N.A. AND VARIANTS TRP-54 AND VAL-157.  
RX MEDLINE=94400459; PubMed=10471411;  
PA Ebisawa T., Kajimura N., Uchiyama M., Katoh M., Sekimoto M.,  
Watanabe T., Ozeki Y., Ikeda M., Jodo T., Sugishita M., Iwase T.,  
Kamel Y., Kim K., Shibui K., Kudo Y., Yanada N., Toyoshima P.,  
Okawa M., Takahashi K., Yamuchi T.;  
RT Allelic variants of human melatonin 1a receptor: function and  
RT prevalence in subjects with circadian rhythm sleep disorders.\*;  
PL Biochem. Biophys. Res. Commun. 262:832-837(1999).  
CC This receptor is highly sensitive to melatonin, likely to mediate  
CC the reproductive and circadian actions of melatonin. THE ACTIVITY  
CC OF THIS RECEPTOR IS MEDIATED BY PERUSSIS TOXIN SENSITIVE G  
CC PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HYPOTHALAMIC PARS TUNICATA AND  
CC HYPOTHALMIC SUPRACHIASMATIC NUCLEI (SN). HIPPOCAMPUS  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation.  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed, usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch>)  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
CC  
CC EMBL, U14108, AAB17720.1;  
CC EMBL, A022933; BAA5303.1;  
CC EMBL, A022933; BAA5303.1;  
CC GPR, GPR\_2032;  
CC MIM: 600665;  
CC INTERPRO: IPR000025;  
CC INTERPRO: IPR000026;  
CC INTERPRO: IPR002278;  
CC PDB: PDB0001; 7tm\_1.1;  
CC PDB: PDB0001; 7tm\_1.1;



```

Db 6. LBNAGNIFVVSIAADLVVAIPYPLVLSIFNNNGMNLGYLHCQASNLMLSLVIGSIFN 120
QY 118 ITGIAINRYCYCHSLKDYKLSKNSLCLVLLIMLITLAAVLPNFRAGTQYDPRISYC 177
Db 121 ITGIAINRYCYCHSLKDYKLSKNSLCLVLLIMLITLAAVLPNFRAGTQYDPRISYC 180
QY 178 TFAOSVSSATYIAVAVFHLVPMIIVFCYLRIMLITLAAVLPNFRAGTQYDPRISYC 237
Db 181 TFGOSVSSATYIAVAVFHLVPMIIVFCYLRIMLITLAAVLPNFRAGTQYDPRISYC 240
QY 238 VTMFVVVFLAICAPLNFGLAVASDPASVPRIPFVAVSYMAVNSCLNIIYGL 297
Db 241 VTMFVVVFLAICAPLNFGLAVASDPATMAPRIPEMLFVASYMAVNSCLNIIYGL 300
QY 298 LQNFPRKRYRRIYSLCTARVFFVSSNDVADRVKMKPSPPLMNNVAVDSV 350
Db 291 LQNFPRKRYRRIYSLCTARVFFVSSNDVADRVKMKPSPPLMNNVAVDSV 353

RESULT 3
MLA-MOUSE STANDARD: PRT: 353 AA.
ID 061184:
AC 01-NOV-1997 (Rel. 35, Created)
ET 01-NOV-1997 (Rel. 35, Last sequence update)
ET 01-NOV-1997 (Rel. 35, Last annotation update)
DE MELANOTIN RECEPTOR TYPE 1A (MEL-1A-R).
CN MTNPLA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-BALB/C:
RC MEDLINE-96290986; PubMed-8754776; Reppert S.M.;
RA Roca A.L., Godson C., Weaver D.P.
RT "Structure, characterization, and expression of the gene encoding the
mouse melatonin receptor."
RL Endocrinology 137:3469-3477(1996).
CC -1- FUNCTION. HIGH AFFINITY RECEPTOR FOR MELANOTIN. LIKELY TO MEDIATE
THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELANOTIN. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY PERUSSIS TOXIN SENSITIVE G
PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION. INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY. BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
CC
CC EMBL: U53223; AAB08755.1;
CC GDB: GCR1650; MTNPLA
CC MGI: MGI:102367; MTNPLA
CC INTERPRO: IPR000025;
CC INTERPRO: IPR002276;
CC INTERPRO: IPR002278;
CC PIRAM: P00001; 7tm_1; 1.
CC PRINTS: P000857; MELANOTINR.
CC PRINTS: P000237; G-PROTEIN RECEPTOR FL 2; 1.
CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC PROSITE: PS00262; G-PROTEIN RECEPTOR FL 2; 1.
CC G-protein coupled receptor; Extracellular; Glycoprotein.
CC DOMAIN 1 32
CC TRANSMEM 33 53
CC TRANSMEM 34 66
CC TRANSMEM 67 87
CC TRANSMEM 88 105
CC TRANSMEM 106 126
CC TRANSMEM 3 (POTENTIAL).

```

```

FT DOMAIN 127 145
FT TRANSMEM 146 166
FT TRANSMEM 167 190
FT TRANSMEM 191 211
FT TRANSMEM 212 243
FT TRANSMEM 244 264
FT TRANSMEM 265 277
FT TRANSMEM 278 298
FT TRANSMEM 299 353
FT DISULFID 103 180
FT CARBOHYD 4 10
FT CARBOHYD 10 10
SQ SEQUENCE 353 AA; 39837 MW; 0375C2F41954C74 CPO64;

Query Match 86.5%; Score 1570.5; DB 1; Length 353;
Best Local Similarity 84.1%; Prod. No. 9.2e-85;
Matches 297; Conservative 28; Mismatches 25; Indels 3; Gaps 1;

QY 1 MONGSALPNASQVPL--RGDGRPSWLASALACVLIFFIYVD:LGMLVLSVYPRKK 57
Db 1 MGNVSELLNATQOAPGCGGRPRPSWLASLTAFLITFYVDLGNLNLVLSYPRKK 60
QY 58 LBNAGNIFVVSIAADLVVAIPYPLVLSIFNNNGMNLGYLHCQVSGPLMGLSVIGSIFN 117
Db 61 LBNAGNIFVVSIAADLVVAIPYPLVLSIFNNNGMNLGYLHCQVSAFLMGLSVIGSIFN 120
QY 118 ITGIAINRYCYCHSLKDYKLSKNSLCLVLLIMLITLAAVLPNFRAGTQYDPRISYC 177
Db 121 ITGIAINRYCYCHSLKDYKLSKNSLCLVLLIMLITLAAVLPNFRAGTQYDPRISYC 180
QY 178 TFAOSVSSATYIAVAVFHLVPMIIVFCYLRIMLITLAAVLPNFRAGTQYDPRISYC 237
Db 181 TFGOSVSSATYIAVAVFHLVPMIIVFCYLRIMLITLAAVLPNFRAGTQYDPRISYC 240
QY 238 VTMFVVVFLAICAPLNFGLAVASDPASVPRIPFVAVSYMAVNSCLNIIYGL 297
Db 241 VTMFVVVFLAICAPLNFGLAVASDPATMAPRIPEMLFVASYMAVNSCLNIIYGL 300
QY 298 LQNFPRKRYRRIYSLCTARVFFVSSNDVADRVKMKPSPPLMNNVAVDSV 350
Db 291 LQNFPRKRYRRIYSLCTARVFFVSSNDVADRVKMKPSPPLMNNVAVDSV 353

RESULT 4
MLA-CHICK STANDARD: PRT: 353 AA.
ID P49285:
AC 01-FEB-1996 (Rel. 33, Created)
ET 01-FEB-1996 (Rel. 33, Last sequence update)
ET 01-OCT-1996 (Rel. 34, Last annotation update)
DE MELANOTIN RECEPTOR TYPE 1A (MEL-1A-R) (CKA).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
[1]
RN SEQUENCE FROM N.A.
RP MENDLINE-96073557; PubMed-7516645;
RA Reppert S.M., Weaver D.R., Cassone V.M., Godson C.,
RA Kolakowski L.F. Jr.;
RT "Melatonin receptors are for the birds: molecular analysis of two
receptor subtypes differentially expressed in chick brain."
RL Neuron 15:1003-1015(1995).
CC -1- FUNCTION. HIGH AFFINITY RECEPTOR FOR MELANOTIN. THE ACTIVITY OF
THIS RECEPTOR IS MEDIATED BY PERUSSIS TOXIN SENSITIVE G PROTEINS
THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION. INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY. EXPRESSED IN OPTIC TECTUM AND RETINA. LESS IN
NEOSTRIATUM, HIPOTHALAMUS AND THALAMUS.
CC -1- SIMILARITY. BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

```



FT VARIANT 361 361 I -> V (IN MEL 1A(BETA))  
 SO SEQUENCE 366 AA, 40400 MW, 5386EDDF9710E4A CRC64;

Query Match 82.9% Score 1505; DB 1: Length 366;  
 Best Local Similarity 81.4% Pred No. 5.8e-81;  
 Matches 287; Conservative 29; Mismatches 33; Indels 4; Gaps 3;

QY 2 GNGG-SALPNASQPV--RSDGA--RPSWLASALACVLIFFIVDILGMLVLSYRNKK 57  
 DB 14 KNGSGALLNNGAAGAGADGVPPSPSWLAATLAILFFIIVDILGMLVLSYRNKK 73  
 QY 58 LBNAGNIFVNSLADLVVAIPYELVLMSTNNMNGYHCOVSGGLMGISVGSIFN 117  
 DB 74 LBNAGNIFVNSLADLVVAIPYELVLMSTNNMNGYHCOVSGGLMGISVGSIFN 133  
 QY 118 ITGAINRVCYICHSKYKLYSKNSKSLCYLLIMLLIAVLPMIRAGTLOYDRIYSC 177  
 DB 134 ITGAINRVCYICHSKYKLYSKNSKSLCYLLIMLLIAVLPMIRAGTLOYDRIYSC 193  
 QY 179 TFASSVSSATTAVVVFHFLVPMIYIFCYLFWITVLCVQPVPPPKPKPKPPDPNF 237  
 DB 194 TFGQSSVSSATTAVVVFHFLVPMIYIFCYLFWITVLCVQPVPPPKPKPKPPDPNF 253  
 QY 233 VTFEYVFLFAICMAPLNFGLAVASDPASMPFIPFWLFFVASYMYAFNSCLNIIYGL 297  
 DB 254 VTFEYVFLFAICMAPLNFGLAVASDPASMPFIPFWLFFVASYMYAFNSCLNIIYGL 313  
 QY 299 LNCNPFKFPYPTIVSLCTAVFVVDSSNDVADRVKKKPSPLMNNVNVDSV 350  
 DB 314 LNCNPFKFPYPTIVSLCTAVFVVDSSNDVADRVKKKPSPLMNNVNVDSV 366

RESULT 6  
 MLIC\_CHICK STANDARD; PRT: 346 AA.

AC P49288;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE MELATONIN RECEPTOR TYPE 1C (MEL-1C-R) (CHK)  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neornithae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 FX MEDLINE=96073557; PubMed=7576645.  
 FA Reppert S.M., Weaver D.P., Cassone V.M., Godson G.,  
 FA Kolakowski L.F., Jr.,  
 FT "Melatonin receptors are for the birds: molecular analysis of two  
 FT receptor subtypes differentially expressed in chick brain.";  
 FT Neuron 15:1003-1015(1995).  
 RT  
 CC - FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. THE ACTIVITY OF  
 CC THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTEINS  
 CC THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).  
 CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC - TISSUE SPECIFICITY: EXPRESSED IN OPTIC TECTUM, NEOSTRIATUM,  
 CC HYPOTHALAMUS, THALAMUS AND PINEAL GLAND, LESS IN CEREBELLUM AND  
 CC RETINA.  
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS  
 CC -  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@sib.ch](mailto:license@sib.ch)).  
 CC  
 DR EMBL: U31821; AAA02499.1;  
 DR GDB: GDB:1080;  
 DR INTERPRO: IPR000025;

DR INTERPRO: IPR000276;  
 DR INTERPRO: IPR002279;  
 DR PRAM: PR00001; 7tm.1; 1.  
 DR PRINTS: PRO0857; MELATONINR.  
 DR PRINTS: PRO1150; MELATONINICR.  
 DR PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE: PS02362; G-PROTEIN\_RECEP\_F1\_2; 1.  
 DR PROSITE: PS02362; G-PROTEIN\_RECEP\_F1\_3; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT DOMAIN 1  
 FT TRANSMEM 27 47  
 FT TRANSMEM 48 60  
 FT TRANSMEM 61 81  
 FT TRANSMEM 82 99  
 FT TRANSMEM 100 120  
 FT TRANSMEM 121 139  
 FT TRANSMEM 140 160  
 FT TRANSMEM 161 184  
 FT TRANSMEM 185 205  
 FT TRANSMEM 206 237  
 FT TRANSMEM 238 259  
 FT TRANSMEM 259 271  
 FT TRANSMEM 272 292  
 FT TRANSMEM 293 346  
 FT DISULFID 97 174  
 FT CARBOHYD 7 7  
 SO SEQUENCE 346 AA, 38575 MW, 2430474025A8E23 CRC64;

Query Match 68.6% Score 1244.5; DB 1: Length 346;  
 Best Local Similarity 67.1% Pred No. 6.6e-65; Indels 3; Gaps 1;  
 Matches 233; Conservative 49; Mismatches 62

QY 1 MONGSALPKASQPVLRGQARSPSWLASALACVLIFFIVDILGMLVLSYRNKKLRN 60  
 DB 1 MERRGS---NGSCSGRLEGGRAPARASGLAVALTVTIYDVLGNALVLSYRNKKLRN 57  
 QY 61 AGNIFVNSLADLVVAIPYELVLMSTNNMNGYHCOVSGGLMGISVGSIFNITG 120  
 DB 58 AGNIFVNSLADLVVAIPYELVLMSTNNMNGYHCOVSGGLMGISVGSIFNITG 117  
 QY 121 IAINRVCYICHSKYKLYSKNSKSLCYLLIMLLIAVLPMIRAGTLOYDRIYSCFPA 180  
 DB 118 IAINRVCYICHSKYKLYSKNSKSLCYLLIMLLIAVLPMIRAGTLOYDRIYSCFPA 177  
 QY 161 USVSSATTAVVVFHFLVPMIYIFCYLFWITVLCVQPVPPPKPKPKPPDPNFPTM 240  
 DB 178 QVSTSTYITVVVFHFLVPMIYIFCYLFWITVLCVQPVPPPKPKPKPPDPNFPTM 237  
 QY 241 FVNVFLFAICMAPLNFGLAVASDPASMPFIPFWLFFVASYMYAFNSCLNIIYGLNQ 300  
 DB 238 FVNVFLFAICMAPLNFGLAVASDPASMPFIPFWLFFVASYMYAFNSCLNIIYGLNQ 297  
 QY 301 NFRREYRIIVSLCTAVFVVDSSNDVADRVKKKPSPLMNNVNV 347  
 DB 298 NFRREYRIIVSLCTAVFVVDSSNDVADRVKKKPSPLMNNVNV 344

RESULT 7

MLIC\_XENLA STANDARD; PRT: 420 AA.  
 AC P49219;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE MELATONIN RECEPTOR TYPE 1C (MEL-1C-R).  
 OS Xenopus laevis (African Clawed frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 CC Xenopodinae; Xenopus.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RT TISSUE-SPECIFIC MELANOPHORES;  
 RC MEDLINE=94286591; PubMed=7517042;  
 RX



QY 81 YPLVMSIFNNQNLGYLHCOVSGFLMGLSVISIFNITGLAIRXCYICHSLKDKLVS 140  
 DB 1 YPLATASIVNDQMSLSLHCGJLSTFLMGLSVISIFNITGLAIRXCYICHSLKDKLVS 60  
 QY 141 SKMSLCYVLLWLTLLTAALVPLNLRAGTLOYPRIYSCFFPAQSVASAVTAVVPHLVPK 200  
 DB 61 STSLCYVLLWLTLLTAALVPLNLRAGTLOYPRIYSCFFPAQSVASAVTAVVPHLVPK 120  
 QY 201 IIVFCYLPILWLVLOVROVYKPKRKLKPODEFNFVTFVLAICAPLNFICGLA 260  
 DB 121 LVVIFCYLRIMALVLCVFMVRYKDNKFLKPKDPNPFVFMVYVLAICAPLNFICGLV 180  
 QY 261 VASDPASVMPRIPEMFLVASYVYAFNSCLNAILYGLLNQNFKRPRIIVSLCTANVF 320  
 DB 181 VASDPASVMPRIPEMFLVASYVYAFNSCLNAILYGLLNQNFKRPRIIVSLCTANVF 240  
 QY 321 VDSNDVADPVYKPKSP 337  
 DB 241 VDSNDVADPVYKPKSP 257  
 RESULT 9  
 MLIB\_CHICK STANDARD: PRT: 289 AA.  
 AC P51050:  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE MELATONIN RECEPTOR TYPE 1B (MEL-1B-R) (FRAGMENT).  
 OS Gallus gallus (chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eluteleostomi;  
 OC Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN:  
 RX MEDLINE-96063731; PubMed-7589552;  
 RA Liu F., Yuan H., Sugamori K.S., Hamadanizadeh A., Lee F.T.S.,  
 RA Pang S.F., Brown G.M., Fristupa Z.B., Niznik H.R.,  
 RT "Molecular and functional characterization of a partial cDNA encoding  
 RT a novel chicken brain melatonin receptor."  
 RL FEBS Lett. 374:273-278(1995).  
 CC -1- FUNCTION. HIGH AFFINITY RECEPTOR FOR MELATONIN. THE ACTIVITY OF  
 CC THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTEINS  
 CC THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: BRAIN AND KIDNEY, WITH TRACE LEVELS IN LUNGS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: U03609; AAA85098.1;  
 DR HSSP: P54725; IUBA.  
 DR GPCR: GCR\_1082;  
 DR INTERPRO: IPR000276;  
 DR PFAM: PF00001; 7tm\_1; 1.  
 DR PROSITE: PS00237; G-PROTEIN\_PPCFP\_P1\_3; 1  
 DR PROSITE: PS50243; G-PROTEIN\_PPCFP\_P1\_3; 1  
 KM G-protein coupled receptor; Transmembrane; Glycoprotein.  
 FT NON-ITER 1 1  
 FT DOMAIN 1 2  
 FT TRANSMEM 3 23  
 FT TRANSMEM 24 42  
 FT TRANSMEM 43 62  
 FT TRANSMEM 63 81  
 FT TRANSMEM 82 102  
 FT TRANSMEM 103 126  
 FT DOMAIN 103 126  
 FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 127 147 5 (POTENTIAL).  
 FT DOMAIN 148 179 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 180 200 6 (POTENTIAL).  
 FT DOMAIN 201 233 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 234 254 7 (POTENTIAL).  
 FT TRANSMEM 255 289 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 290 320 BY SIMILARITY.  
 FT DISULFID 321 337  
 SO SEQUENCE 289 AA; 33001 MW; 08F0B3EC1BF3F1 CPG64;  
 Query Match 61.7%; Score 119; DB 1; Length 289;  
 Best Local Similarity 69.9%; Prev No 3e-58;  
 Matches 202; Conservative 42; Mismatches 45; Indels 0; Gaps 0;  
 QY 62 GNIVVSLAADVVAIPYPLVMSIFNNQNLGYLHCOVSGFLMGLSVISIFNITGL 121  
 DB 1 GNIVVSLAADVVAIPYPLVMSIFNNQNLGYLHCOVSGFLMGLSVISIFNITGL 60  
 QY 122 AINRYCYICHSLKDKYSSKNSLCVLLWLTLLTAALVPLNLRAGTLOYPRIYSCFFPAQ 181  
 DB 61 AINRYCYICHSLKDKYSSKNSLCVLLWLTLLTAALVPLNLRAGTLOYPRIYSCFFPAQ 120  
 QY 182 SVSSAYTIAVAVFHLVPMIIVFCYLRIMLVLOVYQVYPPKPKLPODEFNFVTFVLA 241  
 DB 121 SVSSAYTIAVAVFHLVPMIIVFCYLRIMLVLOVYQVYPPKPKLPODEFNFVTFVLA 180  
 QY 242 VVFLVLAICAPLNFICGLVAVSDPASVMPRIPEMFLVASYVYAFNSCLNAILYGLLNQ 301  
 DB 181 VVFLVLAICAPLNFICGLVAVSDPASVMPRIPEMFLVASYVYAFNSCLNAILYGLLNQ 240  
 QY 302 FREYKRIIVSLCTARVFFVDSNDVADPVYKPKSPPLMTNNVYKXDSV 350  
 DB 241 FREYKRIIVSLCTARVFFVDSNDVADPVYKPKSPPLMTNNVYKXDSV 289  
 RESULT 10  
 MLIB\_HUMAN STANDARD: PRT: 362 AA.  
 ID MLIB\_HUMAN  
 AC P49286;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE MELATONIN RECEPTOR TYPE 1B (MEL-1B-R).  
 DE MNR1B.  
 GN MNR1B.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96004613; PubMed-7568007;  
 RA Reppert S.M., Godson C., Mahle C.D., Weaver D.R.,  
 RA Sluogenhapt S.A., Gussella J.F.,  
 RT "Molecular characterization of a second melatonin receptor expressed  
 RT in human retina and brain: the Mel1b melatonin receptor."  
 RL Proc. Natl. Acad. Sci. U.S.A. 92:8734-8738(1995).  
 RN (2)  
 RP SEQUENCE FROM N.A. AND VARIANTS GLD-24 AND PHE-66.  
 RX MEDLINE-20159877; PubMed-10696804;  
 RA Ebisawa T., Uchiyama M., Kajimura N., Kamei Y., Shibui K., Kim K.,  
 RA Kudo Y., Iwase T., Sugishita M., Jodoi T., Ikeda M., Ozeki Y.,  
 RA Watanabe T., Sekimoto W., Katoh M., Yamada N., Toyoshima K., Okawa M.,  
 RA Takahashi K., Yamauchi T.,  
 RT "Genetic polymorphisms of human melatonin 1b receptor gene in  
 RT circadian rhythm sleep disorders and controls."  
 RL Neurosci. Lett. 280:29-32(2000).  
 CC -1- FUNCTION. HIGH AFFINITY RECEPTOR FOR MELATONIN. LIKE MEL-1B,  
 CC THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY  
 CC OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G  
 CC PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN RETINA AND LESS IN BRAIN AND  
 CC HIPPOCAMPUS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announcement/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

EMBL: 025141; AAC50612.1; -  
 EMBL: AB033594; BAA92315.1; -  
 EMBL: AB033597; BAA92315.1; JOINED.  
 GCRDB: GCR\_2003; -  
 MIM: 600804; -  
 INTERPRO: IPR000275; -  
 INTERPRO: IPR000276; -  
 PFM: PFO0001; 7tm\_1; 1.  
 PRINTS: PR00237; GPCPHDOCSN.  
 PRINTS: PR00857; MELATONIN.  
 PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_2; 1.  
 FUNCTION: coupled receptor, transmembrane, glycoprotein, polymorphism.  
 DOMAIN 1 42 1 (POTENTIAL).  
 TRANSMEM 44 63 76 1 (POTENTIAL).  
 TRANSMEM 77 97 97 2 (POTENTIAL).  
 DOMAIN 98 115 1 (POTENTIAL).  
 TRANSMEM 116 135 1 (POTENTIAL).  
 TRANSMEM 147 155 4 (CYTOPLASMIC (POTENTIAL)).  
 TRANSMEM 156 176 4 (POTENTIAL).  
 TRANSMEM 177 209 5 (EXTRACELLULAR (POTENTIAL)).  
 TRANSMEM 209 231 5 (POTENTIAL).  
 TRANSMEM 232 253 6 (CYTOPLASMIC (POTENTIAL)).  
 TRANSMEM 254 274 6 (POTENTIAL).  
 TRANSMEM 275 287 7 (EXTRACELLULAR (POTENTIAL)).  
 TRANSMEM 288 308 7 (POTENTIAL).  
 TRANSMEM 309 362 7 (CYTOPLASMIC (POTENTIAL)).  
 DISULFID 111 190 8 (BY SIMILARITY).  
 CARBOHYD 4 4 4 N-LINKED (GLYCOC. . .) (POTENTIAL).  
 VARIANT 24 24 G->E. /FTID-VAR\_009262.  
 VARIANT 66 66 L->F. /FTID-VAR\_009263.  
 VARIANT 66 66 /FTID-VAR\_009264.  
 SEQUENCE 362 AA. 1018 MW. 83326.42 Da. 121 SP.64.

Query Match 59.98; Score 1088; DB 1; Length 362;  
 Host Local Similarity 51.28; Prod. No. 7.7e-57;  
 Matches 205; Conservative 52; Mismatches 79; Indels 8; Gaps 1.

1 GNSALFNASQVYLKQDCAAPSWLASAGVLTFTVVDILNLLVLSVYNNKRLPNAG 62  
 24 GANSARSP-----PPPPVAVAPASAVLITTAIVAVVNLVII.SVLPNPIPRAG 75  
 63 NIFVSLAVADLVVAIYPRFLVLSIFNNGMNLGYLHCVSGFLMGLEGVIGSFENITIA 122  
 76 NLEIVSLADLVVAIYPRFLVLSIFNNGMNLGYLHCVSGFLMGLEGVIGSFENITIA 135  
 123 LNRCVYGLGLYDGLYSGNSGCVLLIMITIAVLPN.PAGLQDPRTYCTFQSG 182  
 136 LNRCVYGLGLYDGLYSGNSGCVLLIMITIAVLPN.PAGLQDPRTYCTFQSG 195  
 183 VSSAVTAAVYFHLFVMIIVIFCVLIMLVLDQVQPPKPKCKPQCFNFTVAV 242  
 196 ASQVTAAVVVHFLPPIAVAVSCYLPIMVLQAPRAKPKPSPLCLKPSFLMEV 255  
 243 VVIFAIQAPLPIGLAVASDPASVPIPEKLVASYAAVAFNSCLNATLYGLNLF 302  
 256 VVIFAIQAPLPIGLAVASDPASVPIPEKLVASYAAVAFNSCLNATLYGLNLF 315  
 303 KREYRIIVSLTARVFEVSSNDVADVKKRPPSP 337  
 316 KREYRIIVSLTARVFEVSSNDVADVKKRPPSP 350

RESULT 11  
 MLIX\_HUMAN STANDARD; PRI: 613 AA.  
 AC 013585;  
 DT 01-NOV-1997 (Feb 35, Created)  
 DT 01-NOV-1997 (Feb 35, Last sequence update)  
 DT 30-MAY-2000 (Feb 35, Last annotation update)  
 DE MELATONIN-RELATED RECEPTOR (H9).  
 GN GPR50.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PIUITARY;  
 FX MEDLINE:66220098; PubMed:8447486;  
 FA Report S.M., Weaver D.R., Blisawa T., Mahle C.D.,  
 RA Kolchowski L.F. Jr.  
 FT Cloning of a melatonin-related receptor from human pituitary.  
 FT FEBS Lett. 386:219-224(1996).  
 CC -1- FUNCTION: DOES NOT BIND MELATONIN.  
 CC -1- SUBCELLULAR LOCATION: INTERCAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: HYPOTHALAMUS AND PITUITARY.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announcement/> or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

EMBL: 052219; AAC50614.1; -  
 GCRDB: GCR\_1930; -  
 MIM: 300207; -  
 INTERPRO: IPR000276; -  
 PRINTS: PR000276; -  
 PRINTS: PR00151; MELATONIN1X.  
 PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; 1.  
 PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_2; 1.  
 G-protein coupled receptor, transmembrane.  
 DOMAIN 1 30 1 (POTENTIAL).  
 TRANSMEM 31 51 1 (CYTOPLASMIC (POTENTIAL)).  
 TRANSMEM 52 64 2 (POTENTIAL).  
 TRANSMEM 65 85 3 (EXTRACELLULAR (POTENTIAL)).  
 TRANSMEM 86 103 3 (POTENTIAL).  
 TRANSMEM 104 124 4 (CYTOPLASMIC (POTENTIAL)).  
 TRANSMEM 125 143 4 (POTENTIAL).  
 TRANSMEM 144 164 5 (EXTRACELLULAR (POTENTIAL)).  
 TRANSMEM 165 186 5 (POTENTIAL).  
 TRANSMEM 187 209 6 (CYTOPLASMIC (POTENTIAL)).  
 TRANSMEM 210 230 6 (EXTRACELLULAR (POTENTIAL)).  
 TRANSMEM 231 272 7 (POTENTIAL).  
 TRANSMEM 273 294 7 (CYTOPLASMIC (POTENTIAL)).  
 TRANSMEM 295 313 7 (CYTOPLASMIC (POTENTIAL)).  
 DISULFID 101 178 8 (BY SIMILARITY).  
 DOMAIN 315 608 1 (PRO-RICH).  
 SEQUENCE 613 AA. 66024 MW. 96946.74 Da. 1217 SP.64;

Query Match 49.1%; Score 891.5; DB 1; Length 613;  
 Host Local Similarity 49.78; Prod. No. 2.7e-45;  
 Matches 161; Conservative 71; Mismatches 82; Indels 11; Gaps 3;

5 GNSALFNASQVYLKQDCAAPSWLASAGVLTFTVVDILNLLVLSVYNNKRLPNAG 64  
 15 GSKLPQPEVP-----PA-LIIFMCAVITTVVDLIGNSVILAVTRNKKIRNSGNI 65



[illegible][illegible]

FT	DOMAIN	86	103	EXTRACELLULAR (POTENTIAL)
FT	TRANSMEM	104	124	3 (POTENTIAL).
FT	DOMAIN	125	143	CYTOPASMIC (POTENTIAL).
FT	TRANSMEM	144	164	4 (POTENTIAL).
FT	DOMAIN	165	188	EXTRACELLULAR (POTENTIAL)
FT	TRANSMEM	189	209	5 (POTENTIAL).
FT	DOMAIN	210	236	CYTOPASMIC (POTENTIAL).
FT	TRANSMEM	240	260	6 (POTENTIAL).
FT	DOMAIN	261	273	EXTRACELLULAR (POTENTIAL)
FT	TRANSMEM	274	294	7 (POTENTIAL).
FT	DOMAIN	295	375	CYTOPASMIC (POTENTIAL).
FT	DISULFID	101	178	BY SIMILARITY.
FT	CONFLICT	138	138	P -> I (IN REF. 2).
FT	CONFLICT	158	158	L -> M (IN REF. 2).
FT	CONFLICT	218	220	ARD -> D (IN REF. 2).
50	SEQUENCE	575 AA;	62609 MM;	E2C4C1C1F7E2D7E8 CRC64;

Query Match	47.88;	Score 867.5,	DB 1;	Length 575;
Best Local Similarity	48.38;	Pred. No. 6.2e-44;		
Matches 157;	Conservative 73;	Mismatches 84;	Indels 11;	Gaps 3;

```

0Y 5 GSALFNASQVPLKGDGAPSWLASALACVLLFIIVDILGSLNELYLSVYNNKKLRNAGNI 64
   || || || || || || || || || || || || || || || || || || || || ||
Db 15 GOKLPQGPYR-----PA-LIVEMFCAMTIIIVDDIGSMVTLAVSKRRKRRNSGNY 68
   || || || || || || || || || || || || || || || || || || || || ||
0Y 65 FVSLAVADLVVAIYPIPYLVLMSPFNNGNNNGYIHCQVSGFLMLSLVIGSLFNTGAIN 124
   || || || || || || || || || || || || || || || || || || || || ||
Db 66 FVSLAVADLVVAIYPIPYPLMLHMAIGWDLSKQQQVGFITSLVSGSLFNTGAIN 125
   || || || || || || || || || || || || || || || || || || || || ||
0Y 125 RYCYGHSGLKTDKLYSSKNSLCYVLLIQLLTLAVLPLPLPAGTIOYPRISCTFAQSVS 184
   || || || || || || || || || || || || || || || || || || || || ||
Db 126 RYCYGHSCTGHEPFISSVNTCTYLAIVKIMVLAIVPLPMYICITIEYDPRTCTFENYNN 185
   || || || || || || || || || || || || || || || || || || || || ||
0Y 185 SAYTIAVVYFHEFLVPMIIVIFCYLRIMVLVQVQVYKPKPKIKPTGFENFVITMEVF 244
   || || || || || || || || || || || || || || || || || || || || ||
Db 186 PAFATVYCTIHFVPLILLVFCQYVKIMWYFLVAARD--PAGNPNQDLAEVNPFLMEYIF 243
   || || || || || || || || || || || || || || || || || || || || ||
0Y 245 VFACVCAAPLMEIGLAVASDPAVMPPIPEULPFAVSYMAFENSTINAIYGLINQNERK 304
   || || || || || || || || || || || || || || || || || || || || ||
Db 244 LFAVCKCPINLLYLVAVNKRKMAGRKPPNMYLAATIAFNSGLNAVYICVLIENFRP 303
   || || || || || || || || || || || || || || || || || || || || ||
0Y 305 EYPRIVSICITAFVFFVDSNDVAD 329
   || || || || || || || || || || || || || || || || || || || || ||
Db 304 EYWTIFHAMRHPVLELSGLLTDVRE 328
   || || || || || || || || || || || || || || || || || || || || ||

RESULT 13
MLX_MOUSE
ID MLX_MOUSE STANDARD: PRI: 583 AA.
AC 08495:
DT 15-DEC-1998 (Rel. 37, Created)
DT 01-DEC-1998 (Rel. 37, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE MELATONIN-RELATED RECEPTOR (H9).
GN GPR50.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN (1)
RP SEQUENCE FROM N A
PX MEDLINE=99134305; PubMed=9935574;
PA Gubitz A.K., Peppert S.M.;
PT "Assignment of the melatonin-related receptor to human chromosome X
FT (GPR50) and mouse chromosome x (q9r50)";
FL Genes: 55, 248, 251(1999).
CC -1- FUNCTION: DOES NOT BIND MELATONIN.
CC -1- SPECIFIC LATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN-COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC The European Bioinformatics Institute. There are no restrictions on its

```

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.lsb-sib.ch/announce/> or send an email to [license@lsb-sib.ch](mailto:license@lsb-sib.ch)).

CC EMBL: AF065145; AAC21462.1; ALT\_INIT.

DR MD0: M01:1331877; GPR50.

DR INTERPRO: IPR000276; -

DR INTERPRO: IPR002280; -

DR PFM: PFM00001; 7tm.1; 1.

DR PRINTS: P001151; MELATONINR.

DR PROSITE: PS00237; G-PROTEIN\_RECP\_F1\_1; 1.

DR PROSITE: PS00262; G-PROTEIN\_RECP\_F1\_2; 1.

KW G-protein coupled receptor; transmembrane.

FT DOMAIN 1 30 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 31 51 1 (POTENTIAL).

FT DOMAIN 52 64 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 65 85 2 (POTENTIAL).

FT DOMAIN 86 103 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 104 124 3 (POTENTIAL).

FT DOMAIN 125 143 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 144 164 4 (POTENTIAL).

FT DOMAIN 165 188 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 189 209 5 (POTENTIAL).

FT DOMAIN 210 239 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 240 260 6 (POTENTIAL).

FT DOMAIN 261 273 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 274 294 7 (POTENTIAL).

FT DOMAIN 295 583 CYTOPLASMIC (POTENTIAL).

FT DISULFID 101 178 BY SIMILARITY.

SC SEQUENCE 583 AA; 64300 MW; D713500C4R3A2426 CPGC4.

Query Match 47.58; Score 862.5; DB 1; Length 583;  
Best Local Similarity 48.28; Pred. No. 1 2e-43;  
Matches 161; Conservative 71; Mismatches 89; Indels 13; Gaps 4;

QY 5 GSALPNASQPIPTGRTAPPSWIASAIACVLIPTVITGLVITGLVSVNKKLPNAGNT 64  
DB 15 GCKLRKDP-----PA-LIFMFCAMVITVVDLIGNSVILAVTNKKLRNSGNT 65

QY 65 FVNSIAADVAIVAPYPLVMSIFNNGMNLGYLHQVSSFMGLSVISGIFNTGAIN 124  
DB 66 FVNSIAADVAIVAPYPLVMSVGVGMDLSQLOCOMGLVIGLSVSGIFNTGAIN 125

QY 125 RYCTGSLKDYKSKNSLQVLLIMLTLLAVLPNLACGLQVPRRYSCGFQSVS 184  
DB 126 RYCTGSLKDYKSKNSLQVLLIMLTLLAVLPNLACGLQVPRRYSCGFQSVS 185

QY 185 SAVTIAVVEHFLVPMILVIFCYLRLIMLVQLQVQPKPKPKPKPKPKPKPKPKPK 244  
DB 186 PAFVTVICIHFLVPLVIGCYGCKIKIKVLAARD--PAQGNPDNGFAEVRNLTVEVF 243

QY 245 VLAFCAPLNFITGLAVASDPASVPRIPPEMLVASYAMFNSCLNAILIYGLLNQFR 304  
DB 244 VLAFCAPLNFITGLAVASDPASVPRIPPEMLVASYAMFNSCLNAILIYGLLNQFR 303

QY 305 EYRRTVSLCTARVFDSSNDVADRYKMKPSPL 338  
DB 304 EYRTIFHAMKHPILFISHLSDI--RETWETRAL 335

RESULT 14  
MLA\_RAT  
ID MLA\_RAT STANDARD: PRT: 156 AA.  
AC P49218;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DE 01-FEB-1996 (Rel. 33, Last annotation update)  
DE MELATONIN RECEPTOR TYPE 1A (MEL-1A-R) (FRAGMENT).  
GN MTRIA.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia, Eutheria, Rodentia, Scuri-qualit. Muridae, Murinae; Rattus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN:SPRAGUE-DAWLEY; TISSUE-HYPOTHALAMUS, AND PITUITARY;  
RX MEDLINE=95033233; PubMed=7946354;  
RA Reppert S.M., Weaver D.F., Ebisawa T.;  
RT "Cloning and characterization of a mammalian melatonin receptor that mediates reproductive and circadian responses.";  
RL Neuron 13:1177-1185(1994).

CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. LIKELY TO MEDIATES THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY PERUSSIS TOXIN SENSITIVE G PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.  
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -1- TISSUE SPECIFICITY: AT LEAST IN THE BRAIN. MORE PRECISELY IN THE PARS TREPALIS AND THE SUPRACHIASMATIC NUCLEUS.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.lsb-sib.ch/announce/> or send an email to [license@lsb-sib.ch](mailto:license@lsb-sib.ch)).

CC EMBL: 014409; AA57191.1; -  
DR INTERPRO: IPR000276; -  
DR PFM: PFM00001; 7tm.1; 1.  
DR PROSITE: PS00237; G-PROTEIN\_RECP\_F1\_1; PARTIAL.  
DR PROSITE: PS00262; G-PROTEIN\_RECP\_F1\_2; 1.  
KW G-protein coupled receptor; transmembrane; Glycoprotein.

FT NON\_TER 1 1  
FT TRANSMEM 19 39 1 (POTENTIAL).  
FT TRANSMEM 62 82 2 (POTENTIAL).  
FT TRANSMEM 115 135 3 (POTENTIAL).  
FT NON\_TER 156 156  
SC SEQUENCE 156 AA; 18214 MW; 2B5FEA0FB0CBAB1 CPGC4;

Query Match 41.44; Score 751; DB 1; Length 156;  
Best Local Similarity 87.28; Pred. No. 1 3e-37;  
Matches 136; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 127 CYCHSLKDYKSKNSLQVLLIMLTLLAVLPNLACGLQVPRRYSCGFQSVS 185  
DB 1 CYCHSLKDYKSKNSLQVLLIMLTLLAVLPNLACGLQVPRRYSCGFQSVS 185

QY 187 YTIADVVEHFLVPMILVIFCYLRLIMLVQLQVQPKPKPKPKPKPKPKPKPKPK 244  
DB 61 YTIADVVEHFLVPMILVIFCYLRLIMLVQLQVQPKPKPKPKPKPKPKPKPKPK 243

QY 247 PAFVTVICIHFLVPLVIGCYGCKIKIKVLAARD--PAQGNPDNGFAEVRNLTVEVF 282  
DB 121 PAFVTVICIHFLVPLVIGCYGCKIKIKVLAARD--PAQGNPDNGFAEVRNLTVEVF 282

RESULT 15  
MLA\_PIG  
ID MLA\_PIG STANDARD: PRT: 154 AA.  
AC 002781;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUL-1998 (Rel. 36, Last annotation update)  
DE MELATONIN RECEPTOR TYPE 1A (MEL-1A-P) (FRAGMENT).  
GN MTRIA.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-HYPOTHALAMUS, AND PITUITARY;  
RX MEDLINE=9726109; PubMed=9107687;

```

RA Messer L.A., Wang L., Tugale C.K., Yeele M., Chardon P., Pomp D.,
RA Romack J.E., Barendse W., Crawford A.M., Notter D.R.,
RA Rothschild M.F.,
RA "Mapping of the melatonin receptor 1a (MTR1A) gene in pigs, sheep,
RA and cattle."
RL Mamm. Genome 8:368-370(1997).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. LIKELY TO MEDIATES
CC THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY
CC OF THIS RECEPTOR IS MEDIATED BY PEROUSIS TOXIN SENSITIVE G
CC PROTEINS THAT INHIBITS ADENYLYL CYCLASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/nanunc/
CC or send an email to license@sib-sb.ch).
CC -----
DR EMBL: 073326; AAC48726.1; .
DR INTERPRO: IPR000276; .
DR INTERPRO: IPR000345; .
DR PFAM: PF00001; 7tm.1; 1.
DR PROSITE: PS00027; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
DR K-PROTEIN: K50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT NON_TER 1 1
FT DOMAIN <1 19 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 20 40 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 41 62 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 63 83 5 (POTENTIAL).
FT DOMAIN 84 115 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 116 136 6 (POTENTIAL).
FT DOMAIN 137 149 EXTRACELLULAR (POTENTIAL).
FT NON_TER 154 154
FT SEQUENCE 154 AA, 17900 MW, DPE85FR2CS55C93 GPC64;

Query Match 38.6%; Score 700; DB 1; Length 154;
Best Local Similarity 84.4%; Pred. NO. 1.le-24;
Matches 130; Conservative 11; Mismatches 13; Indels 0; Gaps 0

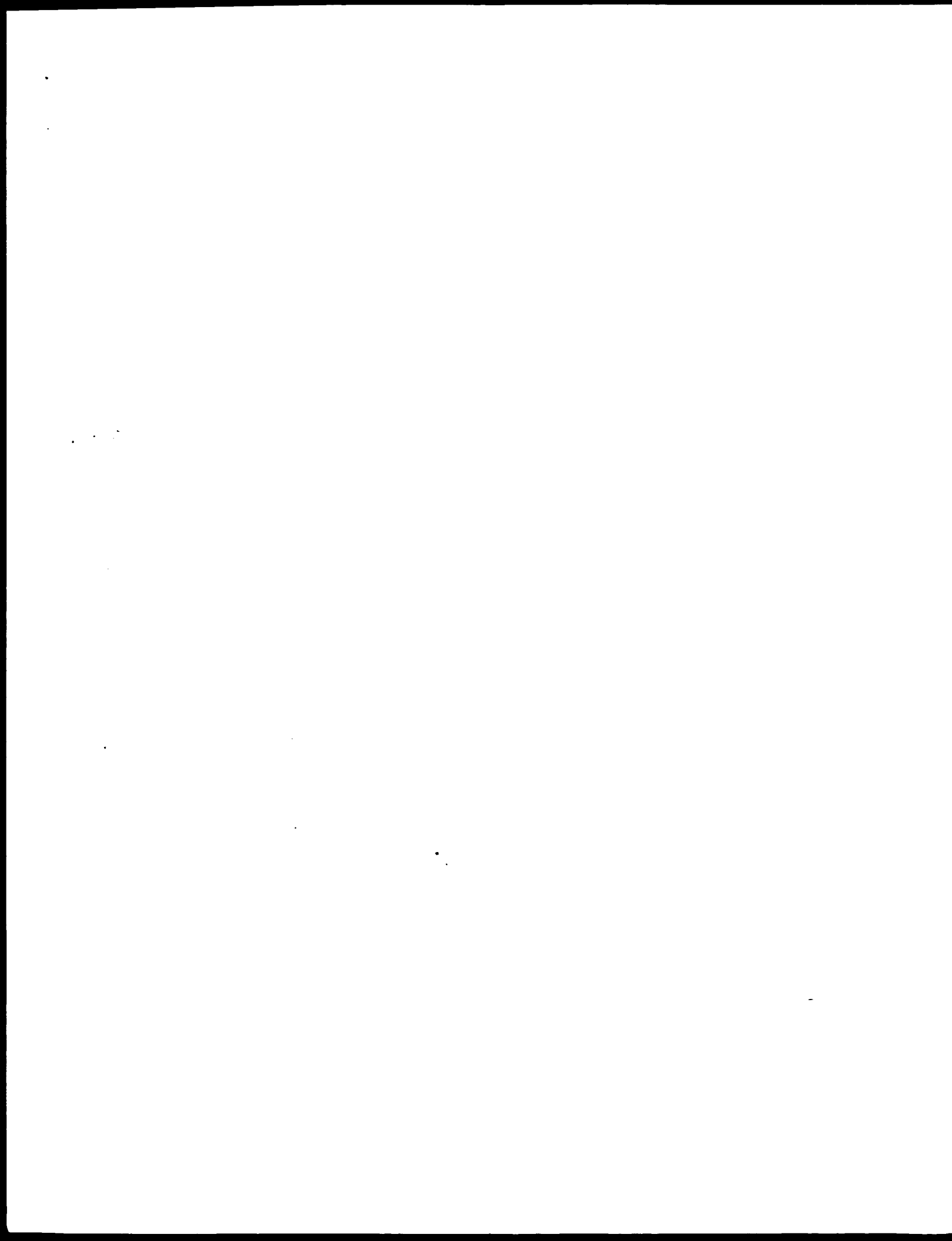
Cy 126 YCYICHSLKYKLVKSSKSLCYVLLMLITLAVALPNIACITLOYDPRISCTFAQSVSS 185
Db 1 YCYICHSLKYKLVKSSKSLCYVLLMLITLAVALPNIACITLOYDPRISCTFAQSVSS 60

Cy 186 AYIAVAVVHFLLVENVYIFCYLRIMIVLVGPDPVAPDRPKLKPDRDFRFTMFEVVF 245
Db 61 AYIAVAVVHFLLVENVYIFCYLRIMIVLVGIIRWAKRKNRPDRPKPDRDFRFTMFEVVF 120

Cy 246 LFAICWAPLNFILGLAVASDPASVMPRIEMDFVA 279
Db 121 LFAICWAPLNFILGLAVASDPASVMPRIEMDFVA 154

```

Search completed. February 18, 2001, 14:36:39  
Job time: 3256 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd

OM protein - protein search, using SW Model

Run on: February 19, 2001, 10:40:32, Search time 77.93 seconds  
(without alignments)  
526,405 Million ppl updates/sec

Title: US-09-226-046-12  
Perfect score: 1815  
Sequence: 1 MGGGSAFLPNASQPLVLRGDG.....VKKPSFLNTNNVYKDVSV 350

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DR seq length: 0

Maximum DR seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: 1: SPREMBL\_15:\*2: sp\_archaea:\*3: sp\_bacteria:\*4: sp\_fungi:\*5: sp\_human:\*6: sp\_invertebrate:\*7: sp\_mammal:\*8: sp\_mhc:\*9: sp\_organelle:\*10: sp\_phage:\*11: sp\_plant:\*12: sp\_ricent:\*13: sp\_virus:\*14: sp\_vertebrate:\*15: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1496	82.6	365	6	Q46608
2	1472	81.1	325	6	Q46608
3	1420	78.2	383	13	Q97289
4	1244	68.5	354	13	Q97289
5	1240	68.3	354	13	Q97289
6	668	36.8	162	13	Q97289
7	644.5	35.5	161	13	Q97289
8	614	33.8	158	13	Q97289
9	597	32.3	154	11	Q97289
10	587	31.3	151	11	Q97289
11	341.5	18.8	392	5	Q9W498
12	341.5	18.8	392	5	Q9W498
13	339	18.7	377	13	Q73733
14	335.5	18.5	392	5	Q9W498
15	331	18.2	420	4	Q9NR49
16	331	18.2	422	4	Q9NR49
17	328.5	18.0	429	5	P92045
18	327	18.0	401	11	Q9R119
19	327	18.0	407	6	Q9W498

Result No.	Score	Query Match	Length	ID	Description
20	326	18.0	375	13	Q57463
21	325.5	17.9	670	5	Q9W534
22	325.5	17.9	670	5	Q9W534
23	323	17.8	400	5	Q9W534
24	323	17.8	508	5	Q9W534
25	322.5	17.8	370	4	Q75194
26	322.5	17.8	404	11	Q9O298
27	322.5	17.8	393	11	Q9R1M0
28	322	17.7	394	5	Q9W721
29	322	17.7	448	11	Q9R0B1
30	322	17.7	444	11	Q9J1Y1
31	320.5	17.7	374	13	Q9W5X1
32	318.5	17.5	398	6	Q9ST44
33	316	17.4	373	13	Q73734
34	313.5	17.3	422	6	Q9TTC9
35	313	17.2	423	4	Q9WYM4
36	313	17.2	424	4	Q9P1V8
37	312.5	17.2	534	13	Q57422
38	311.5	17.2	405	6	Q9XT58
39	311	17.1	518	6	Q9WY18
40	310.5	16.9	405	6	Q9XT57
41	307.5	16.9	388	4	Q9O1Y1
42	307	16.9	380	5	Q9NFV0
43	305.5	16.8	367	13	Q9P1V9
44	304.5	16.8	474	6	Q9T5T6
45	304.5	16.8	474	6	Q9T5T6

## ALIGNMENTS

RESULT 1

ID: Q46608 PRELIMINARY: PRI: 366 AA.

AC: Q46608, 01-JUN-1998 (TREMBL) 06, Created

DT: 01-JUN-1998 (TREMBL) 06, Last sequence update

DT: 01-JUN-2000 (TREMBL) 14, Last annotation update

DE: MEL 1A MELANIN RECEPTOR.

OS: Ovis aries (Sheep).

OC: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.

CC: NCBI TaxID:9940;

OX: NCBI TaxID:9940;

RN: [1]

RP: SEQUENCE FROM N.A.

RA: MEDLINE:9733792; PubMed:9194573;

FX: Barrett P., Conway S., Jockers R., Morgan P.J.,

FA: Guardiola-Lemaitre B., Delaunay J.,

RT: Cloning and functional analysis of a polymorphic variant of the ovine

RI: Mel 1a melanin receptor.

RL: Biochim. Biophys. Acta 1356:299-307(1997).

RN: [2]

RP: SEQUENCE FROM N.A.

RA: Barrett P., Conway S., Morgan P.J.,

FA: Submittal (JAN-1998) to the EMBL/GenBank/DBJ databases.

FX: EMBL: AF045213; AAC0269.1; -

DR: INTERPRO: IPR000025; -

DR: INTERPRO: IPR000276; -

DR: INTERPRO: IPR002278; -

DR: PIR: P00001; 7tm.1; 1.

PFAM: PF00087; MELANINR.

DR: PRINTS: PR00857; MELANINR.

CP: PRINTS: PR00857; MELANINR.

FP: PROSITE: PS00337; G-PROTEIN-RECEPTOR; UNKNOWN.1.

SU: SEQUENCE 366 AA: 40449 MW: 87155CDIFFP299FC CPG64:

Query Match: 2 Q9GSAFLPNASQPLVLRGDG...VKKPSFLNTNNVYKDVSV 350

Best local similarity: 81.3% Pred. No. 4.8e-107; 10-bits 4, Gaps 3;

Matches: 287; Conservative: 27; Mismatches: 95; 10-bits 4, Gaps 3;

```

00014 KQNSVALLNVSAFLAFLASVSPSPSMAIAFLASII:FTIVDELIVNLVLVSVYNNK 7
00015
00016 58 LRKNGNIFVYSLAVADLVAYIIPPVLMLSPFNNGNGLYLRQVSGSLMLSGVSGFEN 117
00017
00018 74 LRKNGVFWVSLAVALLLVAVYPPFLASIVNNGSLSSLRSLSPFLMLSVYSSVSE 132
00019
00020 118 LTGALNPFVYFHSLSKYSKLYSSKNSLQVLLTWLLTAAYFENFATQCYCPFLVSC 177
00021
00022 134 LTGALNPFVYCHSLPFRKYSITNSGLVYFLIMLTLVLAIVPLQVLLVYCPFLVST 194
00023
00024 178 TLAQSSASAVLAAYVHFELVIMLVIVLYLRKMLLVLYVQVQKPKPKPKFLPLQSPFNF 237
00025
00026 194 TFDQSSASVATLAVVHFELVIMLVVYFLIMLVLLVAPKLVKPKPKPKLQSPFNF 254
00027
00028 218 VTFMVEVYFALQMFALNLTSLAVASQFASVFPFEMKFLVASYMAFNSLTVAIVGL 297
00029
00030 254 VTFMVEVYFALQMAFLNLTGLVNASQPDPSAPRIPBMLFVASYMAFNSLTNAIITGL 313
00031
00032 314 LQNFPRQFPRKIIIVSLCTKMFVQSSNVADEIKPKPSLLANRILKLVDSV 366
00033
00034
00035 RESULT 2
00036 09Z280 PRELIMINARY: PRT: 225 AA.
00037
00038 AC 09Z280:
00039 DT 01-MAY-1999 (ITEMHrel: 10, Created)
00040 DT 01-MAY-1999 (ITEMHrel: 10, Last sequence update)
00041 DT 01-OCT-2000 (ITEMHrel: 15, Last annotation update)
00042 DE MELATONIN RECEPTOR MRLA (FRAGMENT):
00043 OS Mesocricetus auratus (Golden hamster):
00044 NC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
00045 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
00046 Mesocricetus.
00047 NCBI_TaxID=10046.
00048 K1
00049 K2
00050 K3 SEQUENCE FROM N.A.
00051 K4 TASSH-SYRPHANGLASMTAT* NQFFIT:
00052 KA 1400 FGL Schuster P., Polrel V., J. Pever P., Masson-Pever M.:
00053 "Cloning cDNAs for the melatonin receptor and demonstrating expression of both melatonin
00054 1 receptor MRLA mRNA and melatonin binding sites in the Syrian hamster
00055 1T suprachiasmatic nucleus".
00056 K5 Brain Res. Mol. Brain Res. 010-04(1998).
00057 DE BRML: AF061158, AAC67241,11: -
00058
00059 DE INTERPRO: IPR000025: -
00060 DE INTERPRO: IPR000276: -
00061 DE INTERPRO: IPR000611: -
00062 DE INTERPRO: IPR002278: -
00063 DE PIRAM: PRD00001: 746:1-1
00064 DE PRINTS: PRD02347: GPCRHD00SN.
00065 DE PRINTS: PRD00857: MELTONINR.
00066 DE PRINTS: PRO01012: NR0P01DEP.
00067 DE PRINTS: PRO01149: MELANININAP.
00068 DE PROSITE: PS00247: G_PROTEIN_RECEPTOR: UNKNOWN_1
00069 KW
00070 K1
00071 K2
00072 K3
00073 K4
00074 K5
00075 K6
00076 K7
00077 K8
00078 K9
00079 K10
00080 K11
00081 K12
00082 K13
00083 K14
00084 K15
00085 K16
00086 K17
00087 K18
00088 K19
00089 K20
00090 K21
00091 K22
00092 K23
00093 K24
00094 K25
00095 K26
00096 K27
00097 K28
00098 K29
00099 K30
00100 K31
00101 K32
00102 K33
00103 K34
00104 K35
00105 K36
00106 K37
00107 K38
00108 K39
00109 K40
00110 K41
00111 K42
00112 K43
00113 K44
00114 K45
00115 K46
00116 K47
00117 K48
00118 K49
00119 K50
00120 K51
00121 K52
00122 K53
00123 K54
00124 K55
00125 K56
00126 K57
00127 K58
00128 K59
00129 K60
00130 K61
00131 K62
00132 K63
00133 K64
00134 K65
00135 K66
00136 K67
00137 K68
00138 K69
00139 K70
00140 K71
00141 K72
00142 K73
00143 K74
00144 K75
00145 K76
00146 K77
00147 K78
00148 K79
00149 K80
00150 K81
00151 K82
00152 K83
00153 K84
00154 K85
00155 K86
00156 K87
00157 K88
00158 K89
00159 K90
00160 K91
00161 K92
00162 K93
00163 K94
00164 K95
00165 K96
00166 K97
00167 K98
00168 K99
00169 K100
00170 K101
00171 K102
00172 K103
00173 K104
00174 K105
00175 K106
00176 K107
00177 K108
00178 K109
00179 K110
00180 K111
00181 K112
00182 K113
00183 K114
00184 K115
00185 K116
00186 K117
00187 K118
00188 K119
00189 K120
00190 K121
00191 K122
00192 K123
00193 K124
00194 K125
00195 K126
00196 K127
00197 K128
00198 K129
00199 K130
00200 K131
00201 K132
00202 K133
00203 K134
00204 K135
00205 K136
00206 K137
00207 K138
00208 K139
00209 K140
00210 K141
00211 K142
00212 K143
00213 K144
00214 K145
00215 K146
00216 K147
00217 K148
00218 K149
00219 K150
00220 K151
00221 K152
00222 K153
00223 K154
00224 K155
00225 K156
00226 K157
00227 K158
00228 K159
00229 K160
00230 K161
00231 K162
00232 K163
00233 K164
00234 K165
00235 K166
00236 K167
00237 K168
00238 K169
00239 K170
00240 K171
00241 K172
00242 K173
00243 K174
00244 K175
00245 K176
00246 K177
00247 K178
00248 K179
00249 K180
00250 K181
00251 K182
00252 K183
00253 K184
00254 K185
00255 K186
00256 K187
00257 K188
00258 K189
00259 K190
00260 K191
00261 K192
00262 K193
00263 K194
00264 K195
00265 K196
00266 K197
00267 K198
00268 K199
00269 K200
00270 K201
00271 K202
00272 K203
00273 K204
00274 K205
00275 K206
00276 K207
00277 K208
00278 K209
00279 K210
00280 K211
00281 K212
00282 K213
00283 K214
00284 K215
00285 K216
00286 K217
00287 K218
00288 K219
00289 K220
00290 K221
00291 K222
00292 K223
00293 K224
00294 K225
00295 K226
00296 K227
00297 K228
00298 K229
00299 K230
00300 K231
00301 K232
00302 K233
00303 K234
00304 K235
00305 K236
00306 K237
00307 K238
00308 K239
00309 K240
00310 K241
00311 K242
00312 K243
00313 K244
00314 K245
00315 K246
00316 K247
00317 K248
00318 K249
00319 K250
00320 K251
00321 K252
00322 K253
00323 K254
00324 K255
00325 K256
00326 K257
00327 K258
00328 K259
00329 K260
00330 K261
00331 K262
00332 K263
00333 K264
00334 K265
00335 K266
00336 K267
00337 K268
00338 K269
00339 K270
00340 K271
00341 K272
00342 K273
00343 K274
00344 K275
00345 K276
00346 K277
00347 K278
00348 K279
00349 K280
00350 K281
00351 K282
00352 K283
00353 K284
00354 K285
00355 K286
00356 K287
00357 K288
00358 K289
00359 K290
00360 K291
00361 K292
00362 K293
00363 K
```

Query Match 81.7% Score 1472.5 DR 11 Length 325  
 Post local Similarity 86.7% Pctd No 4 5e-105  
 Matches 281 Conservative 189 Mismatches 22 Indels 3 Gaps

cy 10 NAGGAPVLR--RGGGAPPSLASATATVTFIVATGTCGATVATSVYRPKKTKRNNAGNFV 66  
 |||||  
 hb 2 NAGGAPVLR--RGGGAPPSLASATATVTFIVATGTCGATVATSVYRPKKTKRNNAGNFV 61  
 |||||

cy 67 VSTAAADLVVALVTPPLVLMSTFFNNGNNGLYGLHCQVSGFLMGLSVIGSTFFNTGTAINRY 128  
 |||||  
 hb 62 VSTAAADLVVALVTPPLVLTSTFNNGNNGLYGLHCQVSAFLMGLSVIGSTFFNTGTAINRY 121  
 |||||

[illegible]

	Query Match	78.24%	Score 1420	DB 13	Length 388
	Best Local Similarity	79.24% <td>Prod. No. 5,448-101</td> <td></td> <td></td>	Prod. No. 5,448-101		
	Motif: 260	Conservative	35	Mismatches	33
				Indels	0
				Gaps	0
QY	22	PSRSLASALACVLTITIVDTICNLVITVYENPKRI	PXKNGIFVWSI	AAVAVIATPY	81
DE	30	PPVAVITITIDDELTITIVVLEISNLIVTSYRKRI	RNNKGFVWSI	IAVALVATPY	89
QY	82	PVLSMSPNNKNDLADQVSEFLMSVSGSFNTGIAINCYQI	CHSLKATDESS	141	
DE	90	PVLSISFKKNTLVVHFGISLFLMSVSGSFNTGIAINCYQI	CHSLKATDESS	141	
QY	142	KNSLGVVLLIMLILAAVLPNLPACTGCTGFFVISTCFAS	VSSAYTIAVVFFHIVM	201	
DE	150	KNSGVVLLIMLILVAVLPNLPASLQVGHVYSCFEESS	ASAYTIAVVFFHILM	206	
QY	202	IVVHGVKMTIVVAVPQVYSEKPPFLFGLSPNVIVVEV	VAIPALDMATNIGLAV	261	
DE	210	IVVHGVKMTIVVAVPQVYSEKPPFLFGLSPNVIVVEV	VAIPALDMATNIGLAV	261	
QY	262	ASTGASVHPIHFWLGVASVYAVANLCLMAIVISLNN	FFREYEPHIVSTIADVHFV	321	



RT Central melatonin receptors in the rainbow trout: comparative  
distribution of ligand binding and gene expression.?"  
RL J. Comp. Neurol. 409:413-424(1999).  
DB EMBL: AF178929; AAD51850.1; -  
DR INTERPRO: IPR000025; -  
DR INTERPRO: IPR000276; -  
DR INTERPRO: IPR002278; -  
DR PIRAM: PR00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCRHDOPSN.  
DR PRINTS: PR00857; MELATONINR.  
DR PRINTS: PR01149; MELATONINAR.  
KW Receptor.  
FT NON-TER 1 1  
FT N-TER 162 162  
FT N-TER 162 162  
SU SEQUNCE 162 AA: 18896 MW: 181809151038AR78 CPG64:

Query Match 36.8% Score 658; DB 13; Length 162;  
Best Local Similarity 72.2%; Pred. No. 60-44; Mismatches 20; Indels 0; Gaps 0;  
Matches 117; Conservative 25;

QY 127 CYCHSHKLYKLYSSNSLQYVLLIMLTLAVALPNEPAGLQYDPPIYSCIFASVSSA 196  
|||||  
DB 1 CYCHSHKLYKLYSSNSLQYVLLIMLTLAVALPNEPAGLQYDPPIYSCIFASVSSA 60  
QY 187 YTTAVVVFHFLVPMIVIFCYLRLIMILVQVQPVPPPKPKPKPTFPNPTVAVVL 246  
|||||  
DB 61 YTTAVVVFHFLVPMIVIFCYLRLIMILVQVQPVPPPKPKPKPTFPNPTVAVVL 120  
QY 247 FAVCMAPLNFICGLAVASDPASVPPPEMFLVASYAYAFNS 288  
|||||  
DB 121 FAVCMAPLNFICGLAVASDPASVPPPEMFLVASYAYAFNS 162

RESULT 7  
Q9JL77 PRELIMINARY: PRT: 161 AA.

DT 01-MAY-2000 (TRENBLREL 13; Created)  
DT 01-MAY-2000 (TRENBLREL 13; Last sequence update)  
DT 01-OCT-2000 (TRENBLREL 15; Last annotation update)  
DE MELATONIN RECEPTOR (FRAGMENT).  
OS Cyathochus mykiss (Rainbow trout) (Salmo gairdneri).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Cyathochus;  
OX NBLTaxID=4022;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE: 99406591; PubMed: 10379923;  
FA Mizutani D., Priestley I., Abulade I., Drew J., Randall C., Bromage N.,  
KA Michael D., Kahn, Williams I. M.;  
RT Central melatonin receptors in the rainbow trout: comparative  
distribution of ligand binding and gene expression.?"  
RL J. Comp. Neurol. 409:413-424(1999).  
DR EMBL: AF178929; AAD54384.1; -  
DR EMBL: AF178929; AAD54384.1; -  
DR INTERPRO: IPR000025; -  
DR INTERPRO: IPR000276; -  
DR PIRAM: PR00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCRHDOPSN.  
DR PRINTS: PR00857; MELATONINR.  
KW Receptor.  
FT NON-TER 1 1  
FT N-TER 161 161  
FT N-TER 161 161  
SU SEQUNCE 161 AA: 18896 MW: 1838398512FAA3 CPG64:

Query Match 35.5% Score 644.5; DB 13; Length 161;  
Best Local Similarity 71.5%; Pred. No. 370-42;  
Matches 116; Conservative 24; Mismatches 21; Indels 1; Gaps 1;  
QY 127 CYCHSHKLYKLYSSNSLQYVLLIMLTLAVALPNEPAGLQYDPPIYSCIFASVSSA 196  
|||||

DB 1 CYCHSHKLYKLYSSNSLQYVLLIMLTLAVALPNEPAGLQYDPPIYSCIFASVSSA 60  
QY 187 YTTAVVVFHFLVPMIVIFCYLRLIMILVQVQPVPPPKPKPKPTFPNPTVAVVL 246  
|||||  
DB 61 YTTAVVVFHFLVPMIVIFCYLRLIMILVQVQPVPPPKPKPKPTFPNPTVAVVL 120  
QY 247 FAVCMAPLNFICGLAVASDPASVPPPEMFLVASYAYAFNS 288  
|||||  
DB 121 FAVCMAPLNFICGLAVASDPASVPPPEMFLVASYAYAFNS 161

RESULT 8  
Q9JL77 PRELIMINARY: PRT: 138 AA.

DT 01-MAY-1999 (TRENBLREL 10; Created)  
DT 01-MAY-1999 (TRENBLREL 10; Last sequence update)  
DT 01-MAY-2000 (TRENBLREL 14; Last annotation update)  
DE MELATONIN RECEPTOR 1A (FRAGMENT).  
OS Elephas maximus (Indian elephant).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eumetazoa; Proboscidea; Elephantida; Elephas.  
OX NCBI\_TaxID=9783;  
RN [1]  
RP SEQUENCE FROM N.A.  
FA Elavsky N.E., Ernst G.W., Messer L.A., Rothschild M.F.;  
RT Identification of Sequence Tagged Sites in the Asian Elephant  
P1 (Elephas maximus) and the African Elephant (Loxodonta africana).?"  
RL Submitted (Mar-1997) to the EMBL/GenBank/DBJ databases.  
RL FMT: 050477; AAB0768.1; -  
DR EMBL: 050477; AAB0768.1; -  
DR INTERPRO: IPR000025; -  
DR INTERPRO: IPR000276; -  
DR INTERPRO: IPR002278; -  
DR PIRAM: PR00001; 7tm\_1; 1.  
DR PRINTS: PR00237; GPCRHDOPSN.  
DR PRINTS: PR00857; MELATONINR.  
DR PRINTS: PR01149; MELATONINAR.  
KW Receptor.  
FT NON-TER 1 1  
FT N-TER 138 138  
FT N-TER 138 138  
SU SEQUNCE 138 AA: 16116 MW: 16724105643AA3 CPG64:

Query Match 33.8% Score 614; DB 6; Length 138;  
Best Local Similarity 63.3%; Pred. No. 6-40; Mismatches 13; Indels 0; Gaps 0;  
Matches 115; Conservative 10;

QY 134 KYDKLYSSNSLQYVLLIMLTLAVALPNEPAGLQYDPPIYSCIFASVSSA 193  
|||||  
DB 1 KYDKLYSSNSLQYVLLIMLTLAVALPNEPAGLQYDPPIYSCIFASVSSA 60  
QY 194 FHHIVMIVIFCYLRLIMILVQVQPVPPPKPKPKPTFPNPTVAVVL 253  
|||||  
DB 61 FHHIVMIVIFCYLRLIMILVQVQPVPPPKPKPKPTFPNPTVAVVL 120  
QY 254 LNFICGLAVASDPASVPPPEMFLVASYAYAFNS 271  
|||||  
DB 121 LNFICGLAVASDPASVPPPEMFLVASYAYAFNS 138

RESULT 9  
Q9JL8 PRELIMINARY: PRT: 174 AA.

DT 01-OCT-2000 (TRENBLREL 15; Created)  
DT 01-OCT-2000 (TRENBLREL 15; Last sequence update)  
DT 01-OCT-2000 (TRENBLREL 15; Last annotation update)  
DE MT2 MELATONIN RECEPTOR MEL-1B (FRAGMENT).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NBLTaxID=10116;  
RN [1]



RP SEQUENCE FROM N.A.  
 RC STRAIN-MISTAR:  
 RA F01rel.V.J., Pever P., Gauer F.:  
 DT "Pat MT2 melanin receptor partial cDNA."  
 RL Submitted (Apr.1999) to the EMBL/Genbank/Trna databases.  
 DR EMBL: AF141863; AAF66601.1;  
 KW Receptor.  
 FT NON TER 1 174  
 FT NON TER 174  
 SC SEQUENCE 174 AA: 19857 MW: 21DDC0437934E77 CFC64

Query Match 32.9% Score 597, DB 11: Length 174:  
 Best Local Similarity 62.6% Pred. No. 1,7e-38:  
 Matches 109: Conservative 28: Mismatches 37: Indels 0: Gaps 0:

QY 124 VYVTHSLKRYKLVSSKRLQVLLITLITLAVLPNLRAGTIOYPRITYSCFAGSVSS 185  
 1 YNCICHSAHYHACSDMHAPLYISLITLITLAVLPNRFVSGSLSDPRITYSCFAGTOST 60  
 QY 186 ATTAIVAVVHFVLPVPIYIFCYLRIMITVLQVPRQVKKDPRKPKIPDPNFVTFVTV 245  
 61 VITMAVAHFLFLFAVVSFCYISFVITVAVGNAPKAKAEPLPLPSTLPSFLIMFAVTV 120  
 QY 246 LEAICWAPLNTGLAVASQASQVPRIPEDMLFVASYVAVYNSCLMAYIGLIN 299  
 121 VFAICWAPLNTGLAVAINPRAMALQIPEDGLVTSYFLAVYNSCLMAYIGLIN 174  
 DB

RESULT 10  
 ID P70329 PRELIMINARY: PRT: 121 AA.  
 AC P70329:  
 DT 31-FEB-1997 (TREMURel. 02, Created)  
 DT 01-FEB-1997 (TREMURel. 02, Last sequence update)  
 DT 01-OCT-2000 (TREMURel. 15, Last annotation update)  
 DE ME-19 MELANIN RECEPTOR (PRACMENI).  
 EE MUS MUSCULUS (Mouse). Chordata: Crustacea: Vertebrata: Euteleostomi:  
 CC Euteleostomi: Melastota: Chordata: Crustacea: Vertebrata: Euteleostomi:  
 CC Mammalia: Euteleostomi: Chordata: Crustacea: Vertebrata: Euteleostomi:  
 CC NCBI\_TaxID=10090.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57/BL6:  
 RA Weaver D.R., Liu C., Peppert S.M.:  
 RL Submitted (May-1996) to the EMBL/Genbank/EBI databases.  
 DR EMBL: U57554; AAB17865.1;  
 DR INTERPRO: IPR000025;  
 DR INTERPRO: IPR000276;  
 DR PFAM: PF00001; 7tm\_1; 1  
 DR PRINTS: PRO0857; MELANINR.  
 DR NON TER 1 121  
 DR NON TER 121  
 SC SEQUENCE 121 AA: 14063 MW: A3776CF024D0CB1C CFC64.

Query Match 21.3% Score 387, DB 11: Length 121:  
 Best Local Similarity 57.0% Pred. No. 1,3e-23:  
 Matches 69: Conservative 21: Mismatches 51: Indels 0: Gaps 0:

CY 124 VYVTHSLKRYKLVSSKRLQVLLITLITLAVLPNLRAGTIOYPRITYSCFAGSVSS 185  
 1 YNCICHSAHYHACSDMHAPLYISLITLITLAVLPNRFVSGSLSDPRITYSCFAGTOST 60  
 DB 1 ATTAIVAVVHFVLPVPIYIFCYLRIMITVLQVPRQVKKDPRKPKIPDPNFVTFVTV 245  
 QY 186 ATTAIVAVVHFVLPVPIYIFCYLRIMITVLQVPRQVKKDPRKPKIPDPNFVTFVTV 245  
 61 VITMAVAHFLFLFAVVSFCYISFVITVAVGNAPKAKAEPLPLPSTLPSFLIMFAVTV 120  
 DB 246 L 246  
 DB 121 V 121

RESULT 11  
 ID Q9W498 PRELIMINARY: PRT: 386 AA.  
 AC Q9W498:  
 DT 01-MAY-2000 (TREMURel. 13, Created)  
 DT 01-MAY-2000 (TREMURel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMURel. 14, Last annotation update)  
 DE CG3171 PROTEIN.  
 GN CG3171.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 CC NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY:  
 RA MEDLINE:20196006; PubMed:10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans G.A., Gockyne T.D.,  
 RA Amandides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle P.F.,  
 RA George P.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sullivan G.C., Mortman J.P., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brannan P.C., Rogers Y.H.C., Blazer P.G., Champagne M., Pfeiffer B.,  
 RA Wan K.H., Boyle C., Baxter K.G., Heit G., Nelson G.P., Miller S.,  
 RA Anell J.F., Abayani A., An H.-J., Andrews-Finkbein C., Egan J.,  
 RA Bailley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari T., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,  
 RA Burtis K.C., Busan D.A., Butler H., Calieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunov R.C., Dunn E.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.I., Harvey D., Heiman T.J., Hernandez J.P., Honick J.,  
 RA Hectin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwa C.,  
 RA Jajami M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp P., Lai Z.,  
 RA Lasko F., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobley R., Murphy L., Murry D.M., Nelson D.L.,  
 RA Mount S.K., Nelson K.A., Nixon K., Nusskern D.R., Paclet M.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.P.S., Scheeler F., Shen H.,  
 RA Shue B.C., Sinden-Klamos T., Simpson M., Skupski M.P., Smith T.,  
 RA Spier R., Tector C., Turner R., Venier E., Wang A.H., Wang X.,  
 RA Svirskas R., Wattam L.A., Weisslock G.M., Weisslock J.,  
 RA Wang Z.-Y., Wasserman U.A., Weislock G.M., Weisslock J.,  
 RA Williams S.M., Woodgate T., Wolley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh K.-F., Zaveri J.S., Zhu M., Zhang C., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 PI "The genome sequence of Drosophila melanogaster."  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003435; AAF46059.1;  
 DR EMBLBASE: FBN0029786; CG3171;  
 DR EMBLBASE: FBN0029786; CG3171;  
 DR INTERPRO: IPR000276;  
 DR PFAM: PF00001; 7tm\_1; 1  
 DR PRINTS: FRC0237; GPCRPRODPSN.  
 DR PRINTS: FRC0237; GPCRPRODPSN.  
 SC SEQUENCE 386 AA: 43105 MW: 98775CF0F0F07704 CFC64.

Query Match 18.8% Score 341.5, DB 5: Length 386:  
 Best Local Similarity 25.8% Pred. No. 1,2e-18:  
 Matches 84: Conservative 68: Mismatches 123: Indels 41: Gaps 9:

CY 27 ASALAVIIFTIVDILGNLVLVSYRNKLR-NAGNIFVSVLAVADLVVAIYPPVYL 85  
 DB 32 AASACVFTVIGVIGNLTLLALKSPTRREHATFAVLSLSLDCSFLPLTA 88



```

DB 153 -SVPANVAVILVWLVAVYSLPLAFHLLISEPYSLEFAPLSOLOVCEVWFSQHRKA 211
QY 187 YTVAVVVFELVEMIVICVYLFIMLVYQVQPVKPRPKPLKQDPENF-----VT 239
DB 212 YTTSLLEFYCCPLLMILYLPF-LPQPFPMLEPQSNPPEDHPRVHSEKFINW 270
QY 240 MEVVFVFAICMAPLNFICLAVASDPASVPRIPEWLFVASYMAVFNCLNAITGLIN 299
DB 271 LATLVAFVAVCMPLINAEVNAVACDQEVLPVGNHLLFSLCHLAMSSTCVNPIYGFIN 330
QY 300 QNPKREYPRITV 311
DB 331 SNPKDVASVVL 342

RESULT 14
Q9NRK26 PRELIMINARY: PRT: 392 AA.
AC Q9NRK26: 01-OCT-2000 (TREMblrel, 15, Created)
DT 01-OCT-2000 (TREMblrel, 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel, 15, Last annotation update)
DE TREHALOSE RECEPTOR 1.
GN TRE1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N. A.
RA Ishimoto H.;
RT Molecular and genetic identification of a taste receptor gene for
RT trehalose in Drosophila.
PI Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
KW EMBL: AB034204; BAA95933.1;
DR Receptor.
SO SEQUENCE 392 AA: 43927 MW: 1607A1C55D4C09E8 CRC64;

Query Match 18.2% Score 335.5 DB 5. Length 392.
Best Local Similarity 26.1% Pred. No. 3.5e-18;
Matches 85; Conservative 64; Mismatches 119; Indels 55; Gaps 10.
QY 27 ASALACVLTIVVDILGNLVLSVYRNKKLR-MNGNIFVGLAVADVAIYPRIVL 85
DB 39 AATSAQVF---VTVGAGNLTLLALCKSPTEBHATIAFVLSLSQILFCSFSLPLTA 94
QY 86 MSIFNNGMNLGYLHGVVSGLMGLSVIGSFNITGAINRYCYI-CHSLKYDKLYSSKNS 144
DB 95 VPFQGESMTFGTTLCKIFPIVIFGNVAVSLSMVGITLNRYLIAHS-RYSQIYKPKFI 153
QY 145 LQVLLMLLTLAVLENRA--GILQYDRIRYSCIFAGSVSSATIAVVFVFLVKKI 202
DB 154 TLGLLFMAVVSFLLLPPIIGIWEMGLDEATESCITLKEGFSIKKTIPIVIGFLPOLV 213
QY 202 VIFCYEPIWITVYGVQPVKPRPKPLKQDPENF----- 237
DB 214 IYVSYSCTIVY-----FHKKKKIKNH--NFIIAAKSSSSSGOSYMTTITPNA 263
QY 238 -----VTMEVVFVFAICMAPLNFICLAVASDPASVPRIPEWLFVASYMAVFNCL 290
DB 264 PEDNPLTVMVYTIPLGLVGFPL-MLANVVDPRNTPSP-----WHTIASVMAVSSVI 318
QY 291 NATIYGLNQRREYRIIVSL 313
DB 319 NPITYAASNRVAVYKIFALL 341

RESULT 15
Q9NR49 PRELIMINARY: PRT: 420 AA.
AC Q9NR49:

```

```

DT 01-OCT-2000 (TREMblrel, 15, Created)
DT 01-OCT-2000 (TREMblrel, 15, Last sequence update)
DT 01-OCT-2000 (TREMblrel, 15, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR HLMAR77
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N. A.
RA Elshourbagy N.A., Ames P.S., Fitzgerald L.R., Foley J.J., Chambers J.,
RA Seckeris P., Schmidt D.R., Buckley P.T., Dyke G.M., Murdock P.R.,
RA Tan K.R., Shabon N., Nuthallgani P., Wang D.Y., Wilson S.,
RA Bergsma D.J., Sarau H.M.;
RT "Cloning and characterization of the human HLMAR77, a G-protein
RT coupled receptor."
PI Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
KW EMBL: AF257210; AAF87078.1;
DR Receptor.
SO SEQUENCE 420 AA: 46866 MW: 7A47C4CEC1DE07 CRC64;

```

```

Query Match 18.2% Score 331; DB 4; Length 420.
Best Local Similarity 26.1% Pred. No. 8.3e-18;
Matches 91; Conservative 76; Mismatches 131; Indels 50; Gaps 11;
QY 34 LFTIVVDILGNLVLSVYRNKKLRNAGNIFVGLAVADVAIYPRIVLMSIFENNGW 93
DB 54 LIFELC--WNGNTVACPLVMNKKHMTVTLFINLAISDLGLGFCMPTLIDNIAGW 111
QY 94 NLGYLHCVCVGLMGLSVIGSFNITGAINRYCYI-CHSLKYDKLYSSKNSLCYVLLIW 153
DB 112 PFGNKKKISGLVAGISVAVETLVAIVDPFGCVVYPER-PKL-TIKIAFVIMITW 169
QY 154 LTLAALVN-----LPAGCLQIDPPRYSTP---AGVSASATIAVVFVFL 197
DB 170 LAITMSPSAVMLHVOEKYFVFLNSCKTSPYWCPEEMPNGEMKITYTVLFANIVL 229
QY 198 VPMIVIFCYLPIWLVY-----GVPGVFKPRPKPKI-KQDPFNFVETMEVFL 246
DB 220 AFLSLIVMYGFGISLHKAVPIHQPKNELEGMVVFPRKY-----TVMILVATL 282
QY 247 FAICMAPLNFICLAVASDPASVFR---PEWLFVASYMAVFNCLNATYGLNQNF 302
DB 283 FLSWELP--WTLMKLSYADLSNRELQIINITYIPAHWLAFGNSSVNPITYGFENMF 340
QY 302 PREYPRIT-VSLGTAPVFPVDSNNVADPVKKRPSPLMTNNVYKVS 349
DB 341 RRGFEAFQLOLQCKRPAKME-----AYALNAKSHVLINTSNQIVQES 383

```

Search completed: February 18, 2001, 16:46:33  
 Job time: 8251 sec













167 tleughn ..... TyrAsProAlaGlyIleTyr..... SerValThrP 179  
494 ATTTCAGATATTTCACAAACAACCTTTCTGCATTCCGAAGGAGAAGATGTATT 445  
179 baAlaGlnSerValSerSerAlaTyrrHLeAlaValAlaValPheHis 195  
444 TTTCAGATGGCTCGCTCAACTACAGCAGCTCATATCTTTCTGTTTTAT 395  
196 PheLeuValProMetLilelleValallePheGlySTyLeuAqIleTrpII 212  
394 ..... ATTCAGAGATATCATGTATGATCAGATTATACGTGGAACATTTCTT 351  
212 eLeuVal ..... LeuGlnValArgGlnArvallylProAspA 225  
350 TGTGGCAAGAACACAAATTCCTCAGCATTCAGAAATACAGACAGCATGACAT 301  
225 rAlserPolySLeouysProGlnAspPheArgAsnPheValThmetPhe 241  
300 CAACCAGACATTATACTAAAAACAGACAAAACGCCAAACTGTATT 251  
242 ValValPheValLeuPheAlaIlePcYSTRPalAProLeuAsnPheIleGI 258  
250 GTATCATACAGACATTTCTTTATATCTTGACCTCA ..... CTATT 210  
258 yLeuAlaValAlaSerAspProAlaSerMetValProAqIleProGluT 275  
209 TCCTGTGATCATCATGATCCTTTTCTTCAGCTACCGCA ACAAAGATG 163  
275 rPLeuPheValAlaSerTYrTYrMetAlaTyrrPheAsnSerCYLeuAsn 291  
162 CATGTTTCAAACATTCCTATGGCTAGGTTATVGAATTCATCACATAAC 113  
292 AlalleleTyrgLyLeuLeuAsnGlnAsnPheArgLYscLoUrtyrArgAr 308  
112 CCTCTCATATACCATTTTTCACAGCTGCTTCGAAGCGCTTT ... 68  
308 gIelleValSerLeucystHraAlaValIlePheValAspSerScTA 325  
67 ..... IICCTGTTGCTTCAGAAAGCTTTTAAAGAGATATGTCAA 25  
325 sn 325  
24 AC 23

seq\_name: qb\_gss27:CNS0412W

seq\_documentation\_block.

LOCUS CNS0412W 882 bp LNA GSS 21-MAY-2000

DEFINITION Heliodon nigroviridis genome survey contig 77 end of clone

FEATURES  
1..1050 of library G from Tetradon nigraviridis genomic survey sequence.  
ACCESSION AF291713  
VERSION AF291713.1 GI 8090294  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetradon nigraviridis.  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eurypterygii; Neopterygii; Teleostei; Euteleostei; Neoclestei;  
Acanthopterygii; Clenogamata; Acanthomorpha; Euacanthomorpha;  
Holacanthopterygii; Acanthopterygii; Perciformes;  
Tetraodontiformes; Tetraodonidae; Tetraodonlinae; Tetradon.  
REFERENCE 1 (bases 1 to 882)  
Roesel-Orellana,H., Jallion,C., Dasilva,C., Fizeser,C., Fischer,C.,  
Bonneau,L., Billault,A., Quelier,F., Saurin,W., Bernot,A. and  
Weissenbach,J.  
Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish tetradon nigraviridis  
Unpublished  
2 (bases 1 to 882)  
Roesel-Orellana,H., Jallion,O., Dasilva,C., Bonneau,L., Fischer,C.,  
Bernot,A., Fizeser,C., Winkler,P., Brotlier,P., Quelier,F.,  
Saurin,W. and Weissenbach,J.







779 TAAACCTAAGACAGACAGTGAATATGAGGCTTGTATGATCGTGTGT 730  
 104 ..... GlypheLeuMetg 108  
 729 TTTCTCTCTCTGACAGGCTCTGCTTGTAGCGCTTACAGCTCTCT 680  
 108 LyeuSerValIleGlySerIlePheAsnIleThgIylleAlaIleAsn 124  
 679 CTCTGTACTGACAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 630  
 125 ArgTyrCysTyrIleCysHisSerIleuLysTyrAspLysLeuTyrSer 141  
 629 CGGTACCATTCATCATGAGCTCTGCTGCTGCTGCTGCTGCTGCTG 580  
 141 rLysAsnSerLeuCysTyrValleuLeuIleTyrLeuLeuThrLeuAla 158  
 579 GTGGCGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 530  
 158 LysAlleuProAsnLeuArgAla... GlyThrLeuGlnTyrAspProArg 173  
 529 CCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
 174 IleTyrSerCysThrPheAlaGlnSerValSerSerAlaTyrThrIleAl 160  
 479 ATGTACAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 430  
 190 AlaValAlaPheHisPheLeuValPheMetIleIleValIlePheCysT 207  
 429 TGTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 380  
 207 YrLeuAsnIleTyrIleLeuValleuAlaValAsnAlaValLysPro 223  
 379 ATGTGACATCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 330  
 224 AspArgLysProLys... LeuLysProGlnAspPheArgAspPhe... ValT 239  
 349 GTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 280  
 239 HmerPheValValPheValIleu... 246  
 279 TGTGTCTCTCTGACAGTACTGCTGCTGCTGCTGCTGCTGCTGCT 230  
 247 ..... PheAlaIleGlyStrpAl 252  
 229 TGTCTATCATGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180  
 252 ..... ProLeuAsnPheIleG 258  
 179 CCACATTGGCTATTTCTACAGAGAGATGTTTCCACATCAAGAGAG 130  
 228 LysAlaValAlaAspAsp... PheAlaSerMetValProArgIle 272  
 129 CTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 83  
 272 Phe... GlnTyrPheValAlaSerTyr 291  
 82 CCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 38  
 seq\_name: qb\_est75:BE798784

seq documentation block:  
 LOCUS BE798784 mRNA EST 20-SEP-2000  
 DEFINITION 60158581P1 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:3939741 5',  
 mRNA sequence.  
 ACCESSION BE798784  
 VERSION BE798784.1 GI:102194982  
 KEYWORDS EST  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo  
 REFERENCE 1 (bases 1 to 861)

AUTHORS NIH-MGC <http://www.ncbi.nlm.nih.gov/MGC/>  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov

ISSUE Procurement: Dcl/DTP  
 CDNA Library Preparation: Ling Hong/Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at: [image.llnl.gov](http://image.llnl.gov)  
 Plate: LHCW/89 Row: a Column: 22  
 High quality sequence start: 7  
 High quality sequence stop: 696.  
 Location/Qualifiers  
 1..861  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_id="NIH\_MGC\_7"  
 /tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: lung; Vector: pUC19; Site: 1. XciI, Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAC(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 170 a 281 c 224 g 186 t  
 ORIGIN

alignment\_scores:  
 quality: 216.00 Length: 205  
 ratio: 1.701 Gaps: 5  
 Percent Similarity: 61.951 Percent Identity: 31.220

alignment\_block:  
 US-09-226-046-12 x BE798784

Align seg 1/1 to: BE798784 from: 1 to: 861

10 AsnAlaSerGlnProValLeuArgGlyAspIylAla..... ArgProSe 24  
 133 AACTGAGCGCGCCCTTCACAGGCTCAGACCGGAGCGGACGACGCA 193  
 24 rTyrLeuAlaSerAlaLeuAlaCysValLeuIlePheThrIleValAla 41  
 183 CAC..... AACTACTAAGGACACAGCTGCTCAGCTGCTGCTGCTG 275  
 41 spIleLeuGlyAsnLeuValIleLeuSerValTyrAsnLysTyr 57  
 227 TGTCTCTGCGCAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 275  
 58 LeuArgAsnAlaGlyAsnIlePheValValSerLeuAlaValAlaAsp 74  
 277 CTGCGAGACCGACCACTACTGCTGCTGCTGCTGCTGCTGCTGCT 326  
 74 uValAlaAlaIleTyrProTyrProLeuValLeuMetSerIlePheAsn 91  
 327 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 376  
 91 snGlyTyrAsnLeuGlyTyrLeuHisCysGlnValIleTyrIleLeuMet 107  
 377 GTGAGTGGAAATTCAGCAGATTCAGCTGCTGCTGCTGCTGCTGCT 426  
 108 GlyLeuSerValIleGlySerIlePheAsnIleThgIylleAlaIleAs 124  
 427 GTGATATATGACGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 476

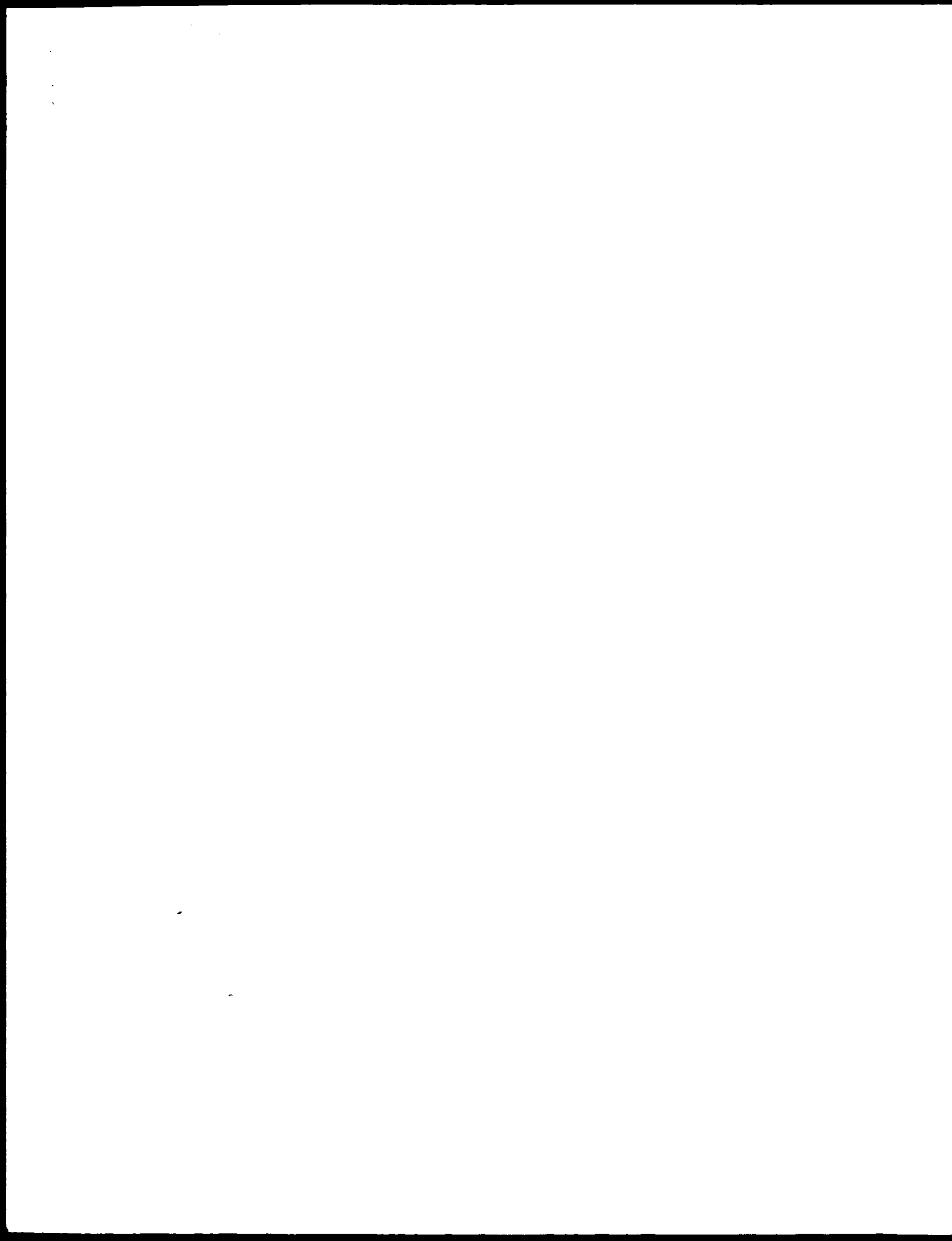








```
Align seq 1/2 to: REF26564 from 1 to: 566
18 GIYASPGIYAlaIarqProSerTrpLeuAlaSerAlaLeuAlaCysValle 34
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
10 GGGAGAGGTGGAGAGAGCCCACTAC AACCTACTATGCCACACTGCT 53
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
34 uIlePheThrIleValAlaSPIleuGIYAsnLeuLeuValIleLeus 51
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
54 CAACCGCTGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
51 ePVAlYrArqAsnLysLysLeuArqAsnAlaGIYAsnIlePheValVa 67
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
104 CTGTGTCCCGCGAGAGCGCGCTGCAGACCAACCACTACTGATCTGC 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
68 SerLeuAlaValAlaAspLeuValAlaIleTYrProTYrProLeuVa 84
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
154 AAGCTGTGAGTGGCGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
84 LleuMetSerIle..PheAsnAsnGIYrPAsnLeuGIYrLeuHisCY 100
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
204 TGTCTACCTGGTAGGCTGGTAGGTGAGTAATTCAGCAGGATTCACGTG 253
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
100 sGIValSerGIYpHeLeuMetGIYLeuSerValIleGIYSerIlePheA 117
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
254 TCACATCTTCTGCTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
117 snIleThrGIYIleAlaIleAsnArqTYrCysTYrIleCysHisSerLeu 133
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
304 ACTGTGTGCTATGAGATGATGATGATGATGATGATGATGATGATGATG 353
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
134 LysTYrAspLysLeuTYrSerSerLysAsnSerLeuCysTYrValLeu.. 149
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
354 CTGTACATACGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 403
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
150 .LeuIleTrpLeuLeuThrLeuAlaAlaValLeuProAsnLeuArgAlaG 166
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
404 CATGCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 450
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
166 IYrThrLeuGIYrAspProArqIleTYrSerCysThrPheAlaGlnSer 182
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
451 GAGCTGATATAGCGGAGAGCAAGAAV..GATGGCATCATCTGCC.... 488
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
183 ValSerSerAlaTYrThrIleAlaValAlaValPheHisPheLeuValFr 199
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
489 ..AACCAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 535
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
199 oMetIleIleValIlePheCysTYrLeuArq 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
536 CTTCATGTGTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 566
```



Tue Feb '20 11:43:02 2001

us-09-226-046-5.rge

Page 1

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2001, 20:17:47 : Search time 3705.49 Seconds  
(without alignments)  
1197.437 Million cell updates/sec

Title: us-09-226-046-5

Perfect score: 867  
Sequence: 1 ggaacacattctgtgtgag.....taaggtgactccgtttaa 867

Scoring table: IDENTITY-NDC  
Gapop 10.0, Gapext 1.0

Searched: 118133 seqs, 2558875103 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

GenEmbl: \*  
1: gb\_dal: \*  
2: gb\_dal: \*  
3: gb\_om: \*  
4: gb\_om: \*  
5: gb\_ph: \*  
6: gb\_ph: \*  
7: gb\_ph: \*  
8: gb\_ph: \*  
9: gb\_ph: \*  
10: gb\_ph: \*  
11: gb\_ph: \*  
12: gb\_ph: \*  
13: gb\_ph: \*  
14: gb\_ph: \*  
15: gb\_ph: \*  
16: gb\_ph: \*  
17: gb\_ph: \*  
18: gb\_ph: \*  
19: gb\_ph: \*  
20: gb\_ph: \*  
21: gb\_ph: \*  
22: gb\_ph: \*  
23: gb\_ph: \*  
24: gb\_ph: \*  
25: gb\_ph: \*  
26: gb\_ph: \*  
27: gb\_ph: \*  
28: gb\_ph: \*  
29: gb\_ph: \*  
30: gb\_ph: \*  
31: gb\_ph: \*  
32: gb\_ph: \*  
33: gb\_ph: \*  
34: gb\_ph: \*  
35: gb\_ph: \*  
36: gb\_ph: \*  
37: gb\_ph: \*  
38: gb\_ph: \*  
39: gb\_ph: \*  
40: gb\_ph: \*  
41: gb\_ph: \*  
42: gb\_ph: \*  
43: gb\_ph: \*

44: em\_hlg8: \*  
45: em\_hlg9: \*  
46: em\_hlg10: \*  
47: em\_hlg11: \*  
48: em\_hlg12: \*  
49: em\_hlg13: \*  
50: em\_hlg14: \*  
51: em\_hlg15: \*  
52: em\_hlg16: \*  
53: em\_hlg17: \*  
54: em\_hlg18: \*  
55: em\_hlg19: \*  
56: em\_hlg20: \*  
57: em\_hlg21: \*  
58: em\_hlg22: \*  
59: em\_hlg23: \*  
60: em\_hlg24: \*  
61: em\_hlg25: \*  
62: em\_hlg26: \*  
63: em\_hlg27: \*  
64: em\_hlg28: \*  
65: em\_hlg29: \*  
66: em\_hlg30: \*  
67: em\_hlg31: \*  
68: em\_hlg32: \*  
69: em\_hlg33: \*  
70: em\_hlg34: \*  
71: em\_hlg35: \*  
72: em\_hlg36: \*  
73: em\_hlg37: \*  
74: em\_hlg38: \*  
75: em\_hlg39: \*  
76: em\_hlg40: \*  
77: em\_hlg41: \*  
78: em\_hlg42: \*  
79: em\_hlg43: \*  
80: em\_hlg44: \*  
81: em\_hlg45: \*  
82: em\_hlg46: \*  
83: em\_hlg47: \*  
84: em\_hlg48: \*  
85: em\_hlg49: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	867	100.0	867	81 AR026630	AR026630 Homo sapi
2	825.2	95.2	149317	58 AC015601	AC015601 Homo sapi
3	823.6	95.0	1085	53 HS014108	HS014108 Homo sapi
4	823.6	95.0	1085	81 AR026631	AR026631 Sequence
5	823.6	95.0	1085	81 E12845	E12845 CDNA encod
6	823.6	95.0	1085	81 AC012209	AC012209 Homo sapi
7	616	70.6	1149	3 OA014109	OA014109 Ovis arie
8	612.4	70.6	1149	3 AR026629	AR026629 Sequence
9	607.6	70.1	1063	11 PS014110	PS014110 Phodopus su
10	604.4	69.7	1219	3 AF045219	AF045219 Mus muscul
11	582	68.1	1063	11 AF061158	AF061158 Mesocricet
12	582	68.1	1063	81 AF061158	AF061158 Mesocricet
13	554.6	62.9	771	3 BT073327	BT073327 Bos taurus
14	543.4	62.7	982	11 AF130341	AF130341 Rattus no
15	543.4	62.7	982	11 AF130341	AF130341 Rattus no
16	497.2	56.4	1065	4 AF156262	AF156262 Oryzomys
17	497.2	56.4	1065	4 AF156262	AF156262 Oryzomys
18	488.8	47.2	1104	4 AF188871	AF188871 Eryx lucif
19	488.8	47.2	1104	4 AF188871	AF188871 Eryx lucif
20	396.4	45.1	1141	4 X1067881	X1067881 Xenopus lae
21	390.6	45.1	1141	4 X1067881	X1067881 Xenopus lae

## ALIGNMENTS

Length 867;

[illegible]













[illegible]

BASE COUNT  
ORIGIN

[illegible]













GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd

OM nucleic - nucleic search, using SW model

Run On: February 18, 2001, 16:49.56 : Search time 121.38 seconds  
(without alignments)  
seqs not aligned with iterations/seq

```

Title: US-09-226-046-5
Perfect score: 867
Sequence: 1 ggaacatcttctgtgtgaq.....taaaqgtgactcgttta 867

```

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters:

	DB	seq	length:
Minimum	DB	seq	0
Maximum	DB	seq	2000000000

Post-processing:	Minimum Match 0%
	Maximum Match 100%

Database

1	/cgm2-2/gcgdata/geneseq/geneseqn/NA19300.DAT *
2	/cgm2-2/gcgdata/geneseq/geneseqn/NA1981.DAT *
3	/cgm2-2/gcgdata/geneseq/geneseqn/NA1982.DAT *
4	/cgm2-2/gcgdata/geneseq/geneseqn/NA1983.DAT *
5	/cgm2-2/gcgdata/geneseq/geneseqn/NA1984.DAT *
6	/cgm2-2/gcgdata/geneseq/geneseqn/NA1985.DAT *
7	/cgm2-2/gcgdata/geneseq/geneseqn/NA1986.DAT *
8	/cgm2-2/gcgdata/geneseq/geneseqn/NA1987.DAT *
9	/cgm2-2/gcgdata/geneseq/geneseqn/NA1988.DAT *
10	/cgm2-2/gcgdata/geneseq/geneseqn/NA1989.DAT *
11	/cgm2-2/gcgdata/geneseq/geneseqn/NA1990.DAT *
12	/cgm2-2/gcgdata/geneseq/geneseqn/NA1991.DAT *
13	/cgm2-2/gcgdata/geneseq/geneseqn/NA1992.DAT *
14	/cgm2-2/gcgdata/geneseq/geneseqn/NA1993.DAT *
15	/cgm2-2/gcgdata/geneseq/geneseqn/NA1994.DAT *
16	/cgm2-2/gcgdata/geneseq/geneseqn/NA1995.DAT *
17	/cgm2-2/gcgdata/geneseq/geneseqn/NA1996.DAT *
18	/cgm2-2/gcgdata/geneseq/geneseqn/NA1997.DAT *
19	/cgm2-2/gcgdata/geneseq/geneseqn/NA1998.DAT *
20	/cgm2-2/gcgdata/geneseq/geneseqn/NA1999.DAT *
21	/cgm2-2/gcgdata/geneseq/geneseqn/NA2000.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	857	100.0	867	17	T09949	High-affinity mela
2	823.6	95.0	1053	20	X05744	Human melatonin re
3	823.6	95.0	1085	17	T09950	High-affinity mela
4	820.6	94.6	1085	18	T60593	Melatonin receptor
5	612.4	70.6	1149	17	T09948	High-affinity mela
6	590	68.1	1296	19	V04644	Mouse melatonin la
7	582	67.1	1062	17	T09951	High-affinity mela
8	389	44.9	1147	18	T79056	Xenopus melatonin
9	389	44.9	1312	18	T79055	Xenopus melatonin
10	384.2	44.3	1147	18	T79063	Xenopus melatonin
11	384.2	44.3	1311	18	T79063	Xenopus melatonin
12	383.8	44.3	1105	17	T09952	High-affinity mela

13	381.2	44.0	1220	17	TC9847
14	64.2	7.4	1440	18	TC8892
15	59.8	6.9	921	18	07324
16	59.8	6.9	921	16	11608
17	59.8	6.9	1567	15	08787
18	59.8	6.9	1567	16	11615
19	59.8	6.9	2719	20	X6115
20	58.4	6.7	960	21	038367
21	58.2	6.7	1798	15	259181
22	58.2	6.7	1798	16	733158
23	56.2	6.7	2084	21	256155
24	56.6	6.5	1788	15	062817
25	54.6	6.3	1086	20	X63747
26	54.6	6.3	1275	19	W05044
27	54.6	6.3	5857	20	224739
28	54.6	6.3	1092	21	245405
29	54.6	6.3	1621	15	072231
30	54.6	6.3	1774	16	111605
31	54.6	6.3	1774	15	086111
32	54.6	6.3	1776	16	111601
33	54.6	6.3	1907	15	066178
34	54.6	6.3	1801	19	V18356
35	54.6	6.3	2094	17	733198
36	54.6	6.3	2140	15	062816
37	54.6	6.3	2140	16	062816
38	54.6	6.3	2140	15	103130
39	54.6	6.3	2140	16	144092
40	54.6	6.3	2140	16	041660
41	51.8	6.0	1880	16	095030
42	51.8	6.0	2108	19	V48285
43	51.8	6.0	2488	17	158943
44	51.8	6.0	2488	20	X24663
45	51.8	6.0	2488	11	004790

XX	Result	1
XX	ID	T09949
XX		T09949 standard; DNA; 867 BP.
AC		T09949;
XX		16-AUG-1996 (first entry)
DE		High-affinity melatonin-1a receptor gene fragment.
XX		Melatonin-1a receptor; human; G-protein-coupled receptor;
KW		melatonin receptor-agonist; melatonin receptor-antagonist;
KW		circadian rhythm disorder; at-lag; day night cycle disorder
KM		ovulation; reproductive cycle; animal breeding; puberty;
XX		antibody; transgenic animal; drug screening; ds.
OS		Homo sapiens.
XX		W09535320-A1.
PN		28-DEC-1995.
PD		07-JUN-1995; 95MC-US07360.
PE		06-JUN-1995; 95US-0319487.
XX		17-JUN-1994; 94US-0261857.
PR		07-OCT-1994; 94US-0319687.
XX		(MASS-) MASSACHUSETTS GEN HOSPITAL.
PA		Reprint SM:
PI		WPI; 1996-058368/06.
XX		P-PSDB; R88411.
XX		



RESOL 3  
T09950  
ID T09950 standard; cDNA; 1085 bp.

D6 216 ggaacaccctccgcgagcggcgca



Db 604 atagcatctctcttactctgaataatgacatctggttccaggtcagacagaggtg 663  
 Oy 478 aaacttaccgcaaaccaactgaacacacagcttcaggaaattttccaccagttt 537  
 Db 664 aaacttaccgcaaaccaactgaacacacagcttcaggaaattttccaccagttt 723  
 Oy 538 gtggttttgcctcttttgcctatttgcctgcttgccttgccttgccttgcctg 597  
 Db 724 gtggttttgcctcttttgcctatttgcctgcttgccttgccttgccttgcctg 783  
 Oy 598 gctctgaccccgccagcatgctgcttgccttgccttgccttgccttgccttgc 657  
 Db 784 gctctgaccccgccagcatgctgcttgccttgccttgccttgccttgccttgc 843  
 Oy 658 taactgagctatttcaacagctgccttgccttgccttgccttgccttgccttgc 717  
 Db 844 taactgagctatttcaacagctgccttgccttgccttgccttgccttgccttgc 903  
 Oy 718 tttaggaagaataacagagaaattatagtttgccttgccttgccttgccttgc 777  
 Db 904 tttaggaagaataacagagaaattatagtttgccttgccttgccttgccttgc 963  
 Oy 778 gacagctctaacagctgccttgccttgccttgccttgccttgccttgccttgc 837  
 Db 964 gacagctctaacagctgccttgccttgccttgccttgccttgccttgccttgc 1023  
 Oy 838 aataatgataaagctgagcttgccttgccttgccttgccttgccttgccttgc 864  
 Db 1024 aataatgataaagctgagcttgccttgccttgccttgccttgccttgccttgc 1050

RESULT 5  
 ID T09948  
 T09948 standard: DNA: 1149 BP.

XX AC T09948:

XX ET 15-AUG-1996 (first entry)

XX TE High-affinity melatonin 1a receptor gene.

XX KM Melatonin-1a receptor: Sheep: G-protein-coupled receptor;  
 KM melatonin receptor-agonist; melatonin receptor-antagonist;  
 KM circadian rhythm disorder; jet-lag; day-night cycle disorder;  
 KW ovulation; reproductive cycle; animal breeding; puberty;  
 KM antibody; transgenic animal; drug screening; ds.

XX OS Ovis aries.

XX FH Key Location/Qualifiers

XX FT CDS 49..1149  
 /tag= a  
 /product= High affinity melatonin-1a receptor

XX PN W09535320-A1.

XX PD 28-DEC-1995.

XX PF 07-JUN-1995: 95WO-US07360.

XX PR 06-JUN-1995: 95US-0319887.

XX PR 17-JUN-1994: 94US-0261957.

XX PR 07-OCT-1994: 94US-0319887.

XX FA (MASS-) MASSACHUSETTS GEN HOSPITAL.

XX PI Reprint SM:

XX DR WPI: 1996-058358/06.

XX DR P-PDR: PA8410

XX PT DNA encoding high affinity melatonin receptor one - used to identify  
 receptor agonists or antagonists e.g. for regulating circadian

PT rhythm disorders or reproductive cycles  
 XX Claim 6, Fig 2, 115pp: English

XX The sequence encodes a sheep high-affinity melatonin receptor,  
 CC which is a membrane protein, coupled to guanine nucleotide binding  
 CC proteins (G-proteins). The gene has been cloned by reverse  
 CC transcription-polymerase chain reaction amplification of sheep pars  
 CC tuberalis mRNA, using primers derived from the Xenopus laevis  
 CC melatonin receptor sequence (T09947), and use of the product as a  
 CC probe on a sheep pars tuberalis cDNA library and a sheep genomic  
 CC library, to obtain the complete sequence as a hybrid fusion with a  
 CC 5'-genomic sequence and a 3'-cDNA sequence. Receptor fragments which  
 CC interact with melatonin, or specific antidiodes, may be used as  
 CC receptor-agonists or receptor-antagonists. Agonists may be used in  
 CC therapy of circadian rhythm disorders such as jet-lag or day-night  
 CC cycle disorders, to control ovulation, or in alteration of  
 CC reproductive cycles in seasonally breeding animals. Antagonists  
 CC may be used to control the initiation or timing of puberty in  
 CC humans. The receptor gene may also be expressed in a transgenic  
 CC animal for use as a model system to screen agonists and antagonists.

SO Sequence 1149 BP: 226 A: 327 C: 318 G: 278 T: 0 other:

Query Match 70.6%; Score 612.4; DB 17; Length 1149;  
 Best Local Similarity 82.3%; Pred. No. 3.8e-165;  
 Matches 716; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

Oy 1 ggaacatcttctggtgagcttgaagctgagctgagctgagctgagcttaccgtac 60  
 Db 280 ggaagatggttctggtgagctgagctgagctgagctgagctgagcttaccgtac 339  
 Oy 61 cccgttctggtgagctgagcttgaagctgagctgagctgagcttaccgtac 120  
 Db 340 cccgttctggtgagctgagcttgaagctgagctgagctgagcttaccgtac 399  
 Oy 121 gtcagtgttctgagctgagctgagctgagctgagctgagcttaccgtac 180  
 Db 400 cttagtgttctgagctgagctgagctgagctgagctgagcttaccgtac 459  
 Oy 181 ggcataccgctgagcttgaagctgagctgagctgagctgagcttaccgtac 240  
 Db 460 ggcataccgctgagcttgaagctgagctgagctgagctgagcttaccgtac 519  
 Oy 241 aagaactccctgagctgagcttgaagctgagctgagctgagcttaccgtac 297  
 Db 520 aagaactccctgagcttgaagctgagctgagctgagctgagcttaccgtac 579  
 Oy 298 aacctccctgagcttgaagctgagctgagctgagctgagcttaccgtac 357  
 Db 580 aacctccctgagcttgaagctgagctgagctgagctgagcttaccgtac 639  
 Oy 358 tccgtcagcttccctgagcttgaagctgagctgagctgagcttaccgtac 417  
 Db 640 tccgtcagcttccctgagcttgaagctgagctgagctgagcttaccgtac 699  
 Oy 418 atagatcttctgagcttgaagctgagcttgaagctgagcttaccgtac 477  
 Db 700 atagatcttctgagcttgaagctgagcttgaagctgagcttaccgtac 759  
 Oy 478 aaactgagctgagcttgaagctgagcttgaagctgagcttaccgtac 537  
 Db 760 aaactgagctgagcttgaagctgagcttgaagctgagcttaccgtac 819  
 Oy 538 gtggttttgcctcttttgcctatttgcctgcttgccttgccttgccttgcctg 597  
 Db 820 gtggttttgcctcttttgcctatttgcctgcttgccttgccttgccttgcctg 879  
 Oy 598 gctctgaccccgccagcatgctgcttgccttgccttgccttgccttgccttgc 657  
 Db 880 gctctgaccccgccagcatgctgcttgccttgccttgccttgccttgccttgc 939





```

XX      T79066; standard: cDNA to mRNA; 1147 BP.
AC
XX      T79066;
XX
XX      10-Nov-1997 (first entry)
XX
XX      Xenopus melatonin receptor MEL-1Ab short form coding sequence.
DE
XX
XX      Alljello: Xenopus laevis: melatonin receptor; untranslated region; PCR:
KW      mpna: half-life: skin amplification; protein polymerase chain reaction;
KW      transmembrane domain; cellular signalling inhibition; adenylyl cyclase;
KW      modulation; intracellular cyclic GMP inhibitor; phosphodiesterase; ss:
XX
XX      Xlaegis: laevis:
XX
XX      Key Location/Qualifiers
XX      CDS     L..1065
XX              /cdd= 3
XX              /product= melatonin receptor MEL-1Ab
XX
XX      W09704094-A1.
XX
XX      06-FEB-1997.
XX
XX      24-JUL-1995; 96MD-PH01167.
XX
XX      24-JUL-1995; 95FR-0008947.
XX
XX      (ADIR ) ADIR & CIF.
XX
XX      Jockers R, Marullo S, Strosberg AD;
XX
XX      WP12:1997-132635/12.
XX
XX      P-PSDR; W25927.
XX
XX      New nucleic acid encoding functional melatonin receptor of Xenopus -
XX      PI for screening for potential (ant)agonists useful for e.g. treating
XX      cardiovascular disease and cancer
XX
XX      claim 1: Page 33-34; 62PP; French.
XX
XX      Sequences 179066-1997 represent novel African genes of the Xenopus laevis
XX      melatonin receptor MEL-1A. The sequences encode proteins which are 65
XX      amino acids shorter than those described in the prior art. This sequence
XX      is a short form of the novel receptor MEL-1Ab also known as
XX      Mol-1-(beta). As compared to the short form (T79066), the difference
XX      occurs in the 3' untranslated region (both sequences encode the same
XX      protein); which is thought to affect the half-life of the mRNA. The
XX      MEL-1Ab sequences also differ from known MEL-1A receptor sequences by
XX      4 amino acids. The nucleotide sequence was isolated from cDNA derived
XX      from Xenopus skin RNA and amplified using the primers T79067-76. The
XX      nucleotide sequence encodes a protein which is a 7 transmembrane receptor
XX      involved in cellular signalling. MEL-1Ab has been shown to modulate
XX      intracellular cAMP, esp. inhibiting its accumulation induced by an
XX      inhibitor of phosphodiesterase, but unlike MEL-1Aa (T79063) cannot
XX      inhibit adenylyl cyclase activity.
XX
XX      Sequence 1147 BP: 41 A; 245 G; 240 C; 348 T; 0 other:
XX
Query Match          44.9% Score 389; DR 18; Length 1147;
Post local similarity 66.6%; Prod No 2 1e-101;
Matches 573; Conservative 0; Mismatches 285; Indels 3; Gaps 1

```

[illegible]



Db 149 ggaattctctttgttcagcttggttcattatgctcattcgtttgtttgtatctccct 258  
QY 61 cccattggtactaatgtccgaattttaacacagctgtggaacctggagctctccacatgccaa 120  
Db 259 ccggtaattccatagaattattcccgaaagggtgtgaagcttggaatatccattgtag 318  
QY 121 gtcaatggtattccatgaaggcccgaaagctgcattgagctccatatccaatccacggcacc 180  
Db 319 atcatgtcttcctgatgagaccagctatttgatcagcttccaacataaacggccta 378  
QY 181 gccatcaacgcctactctttacatctgcacaaagctccaagtcagcaaacgttaagcaga 240  
Db 379 gctatacaacaagtattgtaattctcccaacagcctgagataagaaagcttttaacaa 438  
QY 241 aagaactccctctctctacgtactcctataatgactcgaag---ggcgagcgtctctccc 297  
Db 439 aagaagacctggtcttaacctggtcctgaactgatactacacataatgcatctgcca 498  
QY 298 aacctccatcctggaactctccattacgaagcagagatcattctgtgaccttccccaag 357  
Db 499 aaccttttctgtgatactcaatcaagaccccttgaaatttcttgcacatttaccgaag 558  
QY 358 tccctcaacatcccttatccatccatccctgacatttccactctctctccccaagtc 417  
Db 559 accctaatctcccatcacacacatacaaaatattgttaatgcatatttaaatgcttttagt 618

OY		418	aatacctctctgttacctggaatagatgatccctggcttcacagagfccaagaagaagt	477
Db		619	gtgttgcatctgcgtacttaagaatatggattttaaggaccacaagcaacaagaagt	678
OY		478	aaacctgaccgaacccaactgaactgaacacacagactcaagaattttgtcacagt	537
Db		679	agacaagaactccaagcaaaaagltgacacacaagaacttaagaatttcttacatg	738
OY		538	gtggttttgtccctttttgccatttgtctggctccctgaacttcatttgcttgccgtg	597
Db		739	gtggcttctgactcttttgccttttgcggagccacttgaaatttatcgcttgctgtg	798
OY		598	gacctgccccgcgcagcatgctgacctagaatcccagaatgctgtttgtggccaattac	657
Db		799	gccattaaccaccaccacagcggcaccacaagaatccagaatgtgtgtgtgttaaagctat	858
OY		658	tacatgctgctatttcaaacagctgctctcaatgycattalatcgtgactggaacat	717
Db		859	tctaatgacctattttaaagctgtctcaatgctcactgctcatcagctgtglaataaacac	918
OY		718	ttaaggaagaatacagagaataatatagctctgctctgtacacacagaggtgtttctgtg	777
Db		919	ttcggagaagataatacaacgatatattatgtcccttatgacttgaacttcaagactgtgttctt	978
OY		778	gaacagctcaacagacgttggccacatagagtttaaatggaacacctctccactgtatgaccac	837
Db		979	gacaactccagagagaggaactcagaggtatgaaagaatgagcttgcagcttagaccacac	1038
OY		838	aataatgtagtaaaagctgac	858
Db		1039	aacatccaagcagatatgtac	1059
RESULT	10			
ID	T79064	standard:	CDNA to mRNA:	1147 BP.
XX	AC	T79064;		
XX	DT	10-NOV-1997	(first entry)	
DE		Xenopus melatonin receptor MEL-1Aa short form coding sequence.		
XX	AA	Allele: Xenopus laevis; melatonin; receptor; untranslated region; PCR;		
KW	MPN:	half-life; skin; amplification; primer; polymerase chain reaction		
KW	transmembrane domain;	cellular signalling; inhibition; adenylyl cyclase		
KW	modulation;	intracellular; cyclic GMP; inhibitor; phosphodiesterase; ss		
OS		Xenopus laevis		
XX	Key	Location/Oualifiers		
FH	CDS	1..1065		
FT		/*tag= a		
FT		/product= MEL-1Aa receptor protein		
XX	PD	06-FEB-1997.		
XX	PE	24-JUL-1996;	96WO-FR01167.	
PR	XX	24-JUL-1995;	95FR-0008947.	
FA	XX	(ADIR ) ADIR & CIE.		
PI	XX	Jockers R, Marullo S, Strosberg AB;		
DR	XX	WPI; 1997-132635/12.		
EK	XX	F-ESDS; W25926		
PT		New nucleic acid encoding functional melatonin receptor of Xenopus		
CT		for screening for potential (ant)agonists useful for c.g. treating		
FI		cardiovascular disease and cancer		











Tue Feb 20 11:43:03 2001

us-09-226-046-5.rml

Page 1

Genforce version 4.5  
Copyright (c) 1993 - 2000 Genforce Ltd

OW nucleic nucleic search, using sw model

Run on: February 18, 2001 16:45:36 : Search time 102.05 seconds  
(without alignments)  
1369.191 Million cell updates/sec

Title: US-09-226-046-5

Perfect score: 867

Sequence: 1 ggaacatctctgtgttgaag.....taaaagtgactccatttaa 867

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 28935 seqs, 80580151 residues

Total number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database:

1: Issued Patents\_NA:  
2: /seqs/5/ProdData/2/ina/5A\_GOMR.seq.\*  
3: /seqs/5/ProdData/2/ina/5A\_GOMR.seq.\*  
4: /seqs/5/ProdData/2/ina/5A\_GOMR.seq.\*  
5: /seqs/5/ProdData/2/ina/5A\_GOMR.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	867	100.0	867	2 US-08-466-103A-5	Sequence 5, Appl
2	823.6	95.0	1085	2 US-08-466-103A-11	Sequence 11, Appl
3	612.4	70.6	1149	2 US-08-466-103A-3	Sequence 3, Appl
4	590	68.1	2772	3 US-09-280-420-1	Sequence 1, Appl
5	582	67.1	1062	2 US-08-466-103A-13	Sequence 13, Appl
6	383.8	44.3	1105	2 US-08-466-103A-15	Sequence 15, Appl
7	381.2	44.0	1320	2 US-08-466-103A-1	Sequence 1, Appl
8	59.8	6.9	921	1 US-08-722-001-17	Sequence 17, Appl
9	59.8	6.9	1567	1 US-08-722-001-17	Sequence 24, Appl
10	58.4	6.7	960	3 US-09-130-749-1	Sequence 1, Appl
11	58.4	6.7	960	3 US-09-130-749-1	Sequence 1, Appl
12	58.2	6.7	1738	1 US-08-334-698-3	Sequence 3, Appl
13	58.2	6.7	1738	1 US-08-334-698-3	Sequence 3, Appl
14	58.2	6.7	1738	1 US-08-228-932-3	Sequence 3, Appl
15	58.2	6.7	1738	1 US-08-466-939-3	Sequence 3, Appl
16	58.2	6.7	1738	1 US-08-466-939-3	Sequence 3, Appl
17	58.2	6.7	1738	1 US-08-244-354-3	Sequence 3, Appl
18	58.2	6.7	1738	1 US-09-206-899-3	Sequence 3, Appl
19	58.2	6.7	1738	1 PCT-US95-04203-3	Sequence 13, Appl
20	58.2	6.7	1738	1 PCT-US95-04203-3	Sequence 13, Appl
21	54	6.2	1621	1 US-08-722-001-13	Sequence 13, Appl
22	54	6.2	1776	1 US-08-722-001-29	Sequence 29, Appl
23	54	6.2	1901	1 US-08-153-848-43	Sequence 43, Appl
24	54	6.2	1901	1 US-09-299-843A-43	Sequence 43, Appl
25	54	6.2	2140	1 PCT-US93-11153-43	Sequence 1, Appl
26	54	6.2	2140	1 US-08-334-698-1	Sequence 1, Appl
27	54	6.2	2140	1 US-08-228-932-1	Sequence 1, Appl
28	54	6.2	2140	1 US-08-466-939-1	Sequence 1, Appl

29	54	6.2	2140	3 US-08-722-190-1	Sequence 1, Appl
30	54	6.2	2140	3 US-08-244-354-1	Sequence 1, Appl
31	54	6.2	2140	3 US-09-206-899-1	Sequence 1, Appl
32	54	6.2	2140	3 PCT-US95-04203-1	Sequence 1, Appl
33	54	6.2	2140	3 PCT-US95-07180-1	Sequence 1, Appl
34	51.8	6.0	1280	1 US-08-192-288-1	Sequence 1, Appl
35	51.8	6.0	1280	1 US-08-687-355A-1	Sequence 1, Appl
36	50.8	5.9	7218	1 US-08-232-463-14	Sequence 14, Appl
37	50.4	5.8	1167	1 US-07-960-985-1	Sequence 1, Appl
38	50.4	5.8	1167	1 US-08-496-671-1	Sequence 1, Appl
39	50	5.8	1239	1 US-08-449-036-22	Sequence 22, Appl
40	50	5.8	1239	1 US-08-233-009-22	Sequence 22, Appl
41	50	5.8	1239	1 US-08-560-231-22	Sequence 22, Appl
42	49.6	5.7	1872	1 US-09-080-704A-22	Sequence 22, Appl
43	49.6	5.7	1872	1 US-09-153-848-39	Sequence 39, Appl
44	49.6	5.7	1872	1 US-09-299-843A-39	Sequence 39, Appl
45	49.6	5.7	1872	4 PCT-US93-11153-39	Sequence 39, Appl

#### ALIGNMENTS

RESULT 1  
US-08-466-103A-5  
Sequence 5, Application US/08466103A  
Patent No. 5856124  
GENERAL INFORMATION:  
APPLICANT: Repert, Steven M.  
APPLICANT: Edisawa, Takashi  
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Elie S Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: IBM Compatible  
SOFTWARE: FASTSO for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,103A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/319,887  
FILING DATE: 07-OCT-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/26,857  
FILING DATE: 17-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/MARKET NUMBER: 00786/250002  
TELEPHONE: 617/542-6070  
TELEPHONE: 617/542-6070  
TELEPHONE: 617/542-6070  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 867 base pairs  
TYPE: nucleic acid  
STRANDNESS: double  
TOPOLOGY: linear  
MOLPOUSE TYPE: DNA (genomic)  
FEATURES:  
NAME/KEY: Coding Sequence  
LOCATION: 1..864  
OTHER INFORMATION:  
US-08-466-103A-5











NAME/KEY: Coding Sequence  
 LOCATION: 13..1098  
 OTHER INFORMATION:

US-09-466-103A-15

Query Match: 44.3% Score 383.8; DB 2; Length 1105;  
 Best local similarity 67.1%; Pred. No. 9,7e-94;  
 Matches 567; Conservative 0; Mismatches 272; Indels 3; Gaps 1;

```

UY 1 ggaacatctttagatgagcttagagcagcctgagctgagccttaccctacac 60
DB 235 ggaatattttttagatgagcttagagcagcctgagccttaccctacac 294
UY 61 cgtttatctctatctgacatatttaacacacggttggaaactgagctatctgacac 120
DB 295 cgtttatctctatctgacatatttaacacacggttggaaactgagctatctgacac 354
UY 121 gtcagtgagcttctcattgagcctgagcctgagcctgagccttaccatctgacac 180
DB 455 gtcagtgagcttctcattgagcctgagcctgagccttaccatctgacac 414
UY 181 ggcataacacgctgacatctcaccacacgctgacacacgctgacacacacgacac 240
DB 415 ggcataacacgctgacatctcaccacacgctgacacacgctgacacacacgacac 474
UY 241 aagaactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 297
DB 475 tctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 534
UY 298 aacctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 357
DB 535 aacctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 594
UY 358 tctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 417
DB 595 tctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 654
UY 418 atagatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 477
DB 655 atagatcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 714
UY 479 tctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 537
DB 715 tctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 774
UY 538 atgagcttctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 597
DB 775 atgagcttctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 834
UY 598 ggcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 657
DB 835 ggcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 894
UY 858 tctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 717
DB 895 tctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 954
UY 718 tctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 777
DB 955 tctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1014
UY 778 ggcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 832
DB 1015 ggcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1069

```

RESULT 7  
 US-09-466-103A-1  
 Sequence: 1 Applicant: US-09-466-103A  
 Patent No. 5856124  
 GENERAL INFORMATION:  
 APPLICANT: Reppert, Steven M.

```

1 APPLICANT: Ebisawa, Takashi
2 TITLE OF INVENTION: HIGH-AFFINITY MELANIN
3 TITLE OF INVENTION: RECEPTORS AND USES THEREOF
4 NUMBER OF SEQUENCES: 29
5 CORRESPONDENCE ADDRESS:
6 ADDRESSER: Fish & Richardson P.C.
7 STREET: 225 Franklin Street
8 CITY: Boston
9 STATE: MA
10 COUNTRY: US
11 ZIP: 02110-2804
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Diskette
14 COMPUTER: IBM Compatible
15 OPERATING SYSTEM: Windows95
16 SOFTWARE: Fastseq for Windows Version 2.0
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US-09/466,103A
19 FILING DATE: 06-JUN-1995
20 CLASSIFICATION: 435
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: 08/319,887
23 FILING DATE: 07-OCT-1994
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/261,657
26 FILING DATE: 17-JUN-1994
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Fraser, Janis K.
29 PERMITS/AGENT NUMBER: 34,819
30 REFERENCE/AGENT NUMBER: 007561550002
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: 617/542-5070
33 FAX: 617/542-6006
34 INFORMATION FOR SEQ. ID NO: 1:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 1320 base pairs
37 TYPE: nucleic acid
38 STRANDEDNESS: double
39 TOPOLOGY: linear
40 MOLECULE TYPE: cDNA
41 FEATURE:
42 NAME/KEY: Coding Sequence
43 LOCATION: 32..1291
44 OTHER INFORMATION:
45 US-09-466-103A-1

```

Query Match: 44.0% Score 381.2; DB 2; Length 1320;  
 Best local similarity 66.1%; Pred. No. 5.1e-93;  
 Matches 567; Conservative 0; Mismatches 288; Indels 3; Gaps 1;

```

UY 1 ggaacatctttagatgagcttagagcagcctgagccttaccctacac 60
DB 230 ggaatattttttagatgagcttagagcagcctgagccttaccctacac 289
UY 61 cgtttatctctatctgacatatttaacacacggttggaaactgagctatctgacac 120
DB 290 cgtttatctctatctgacatatttaacacacggttggaaactgagctatctgacac 349
UY 121 gtcagtgagcttctcattgagcctgagcctgagcctgagccttaccatctgacac 180
DB 455 gtcagtgagcttctcattgagcctgagcctgagccttaccatctgacac 409
UY 181 ggcataacacgctgacatctcaccacacgctgacacacgctgacacacacgacac 240
DB 410 ggcataacacgctgacatctcaccacacgctgacacacgctgacacacacgacac 469
UY 241 aagaactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 297
DB 475 tctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 529
UY 298 aacctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 357

```

```

Db 530 AACCTTTTGTGATCAGTACAGTATGACCCAGATTTTTCCTGCACTTTGGCAG 589
Qy 358 tccgcaactccgcaactacacatccgcaactgagtttccactccctcccaatgac 417
Db 590 AAGGTGAGTTCCTATACACATACAGTATGAGTGTGATTTATAGCCCTCTACT 649
Qy 418 atagtcactctctgtaactcgaataatgagctcgtgctccaggtcgaagaagatg 477
Db 650 GTTGATCATCTCTGTTACTTAAAGAAATATGGGTTTAGTGCACAGCAACAGAGT 709
Qy 478 aaaccgaccgcaaaaccacacacacacacacacacacacacacacacacacac 537
Db 710 AGACAGACTTTCAGCAAAAGTTGACACAAACAGACTTGAGAAATTTCTGACCAT 769
Qy 538 gtggttttgcctcttccacttccctcgtcgtcgtcgtcgtcgtcgtcgtcgtc 597
Db 770 GTGGCTTTGTACTTTTGCAGTTGCTGGCCCTTAACTTTATGCGCTTGTGTG 829
Qy 598 gctcctaccccgccagcatgctgctcgaagatcccaagatgctgctgctgctg 657
Db 830 GCCATTATCCCTTTCATGTGGCAGCAAGATTCAGAAATGGCTGTTGTTTAA 889
Qy 658 tacatgacatcttcaacacgctcctcctcctcctcctcctcctcctcctcct 717
Db 890 TTCTATGCTTATTTTACAGTTCTCTCATGCTTATATGCTTATATGCTTATAT 949
Qy 718 ttcaggaagagatagagagatattatgctcgtcgtcgtcgtcgtcgtcgtcgt 777
Db 950 TTCCGCAAGAGGTACAAAGATGCTGATGCTGCTTATTTGACTCCAGACTGTT 1009
Qy 778 gacagctcctacagcagcagcagcagcagcagcagcagcagcagcagcagcag 837
Db 1000 GACACATCTTACAGAGCAACTGAGGAGTTGAAAGTAAAGCTTCCGACGCTGA 1069
Qy 838 aataatgagtaagatg 855
Db 1070 AACATCAAGCAGATATG 1087

```

RESULT 8  
 US-08-722-001-17  
 Sequence 17, Application US/08722001  
 Patent No. 5760054  
 GENERAL INFORMATION:  
 APPLICANT: Thompson, Wayne J.  
 APPLICANT: Huff, Joel P.  
 APPLICANT: Nerenberg, Jennie R.  
 APPLICANT: Lee, Hee-Yoon  
 TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck & Co., Inc.  
 STREET: 126 Lincoln Avenue  
 CITY: Rahway  
 STATE: New Jersey  
 COUNTRY: United States of America  
 ZIP: 07065  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1 ? Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/722,001  
 FILING DATE:  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/229,276  
 FILING DATE: 14-APR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Appolina, Mary A.  
 REGISTRATION NUMBER: 34,087

```

REFERENCE/DOCKET NUMBER: 19169Y
TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
TELEX: 138825
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-722-001-17

```

```

Query Match 6.9% Score 59.8; DB 1, Length 921:
Best Local Similarity 47.8% Pred. No. 4.4e-07:
Matches 206; Conservative 0; Mismatches 222; Indels 3; Gaps 1:

```

```

Qy 4 aacactctgtgtgagcgtttagcgttgcgtgagcgtggtgtgtgtgtgtgtgtgtgt 63
Db 249 AACACTTTCATTTTCACACTGCGCATGCGGACCTGTCTTTAGCTTACCCCTCTG 308
Qy 64 ttgtgtcgtatgctgctatattacacacggtgtgaaacctgtgctatctgcaactc 123
Db 309 TTTCTAGCGGCGCTTACAGAGTGTCTGTGCTACTGCGGTGCTGGGCGGATCTTCT 368
Qy 124 agtggatcttcgtatgagcgttgaagcgttgcgtatcgtcctcattacacacac 183
Db 369 TGGGACCGCGTGAGATGCTGCTGCTGTCACAGCGCTTCTGTAGCCTCTGGCGCAT 428
Qy 184 atcaacccctactgttattacacacacacacacacacacacacacacacacacac 243
Db 429 ATGATGCTGATATGCGGCTGCGTACTGCTGCGATGCTGCGATGCTGCGATGCT 488
Qy 244 aactcctctgtcgtcgtcctcctcctcctcctcctcctcctcctcctcctcctc 303
Db 489 AAGGCATCTTGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 548
Qy 304 cgtcgtggaactcctcgtgagcagcaga---gaatctactcgtgacactctgcccag 360
Db 549 CTCCTTGGGAGAGAGAGCGCCGACCCAAAGATGACAAAGATGCGGCTGCTGAG 408
Qy 361 gtcagctcgcctacacacacacacacacacacacacacacacacacacacacac 420
Db 600 CCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568
Qy 421 gtcactctctg 431
Db 669 GTCATGACTG 679

```

```

RESULT 9
US-08-722-001-24
Sequence 24, Application US/08722001
Patent No. 5760054
GENERAL INFORMATION:
APPLICANT: Thompson, Wayne J.
APPLICANT: Huff, Joel P.
APPLICANT: Nerenberg, Jennie R.
APPLICANT: Lee, Hee-Yoon
TITLE OF INVENTION: ALPHAIC ADRENERGIC RECEPTOR ANTAGONISTS
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: 126 Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07065

```



```

GENERAL INFORMATION:
APPLICANT: SHARON, USMAN
AFFILIANT: ELSHOPBAGY, NARIL
TITLE OF INVENTION: MOLECULAR CLONING OF A 71M
TITLE OF INVENTION: RECEPTOR (GPR31A)
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: RAINER & PRESTIA
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,749
FILING DATE: 07-AUG-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F.
REGISTRATION NUMBER: 29,093
REFERENCE/DOCKET NUMBER: GP-70913
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 960 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-130-749-1

Query Match          5.7%; Score 58.4; DB 3; Length 960;
Best Local Similarity 50.4%; Pred. No. 1.1e-06;
Matches 143; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

```

```

APPLICANT: Jonathan A. Bard et al.
TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenergic
TITLE OF INVENTION: Receptors and Uses Thereof
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/334,698
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/952,798
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28 678
REFERENCE/DOCKET NUMBER: 376901
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: N
ANTI-SENSE: N
FEATURE:
NAME/KEY: CDS
LOCATION: 124..1683
OTHER INFORMATION:
US-08-334-698-3

Query Match          6.7%; Score 58.2; DB 1; Length 1738;
Best Local Similarity 47.6%; Pred. No. 1.5e-06;
Matches 205; Conservative 0; Mismatches 223; Indels 3; Gaps 1;

```





Query Match	6.7%	Score 58.2;	DB 1;	Length 1733;
Best Local Similarity	47.6%;	Pred. No. 2.5e-06;		
Matches 205;	Conservative	0;	Mismatches 223;	Indels 3;
				Gaps 1

[illegible]

QY	124	atgaggctccctatgagcctagagctatcgctccatcatctcaatcaacagcgacacgc	183
Dh	484	TGAGGCAAGCGTGGATGTCCTGAGCGACAGCGCCGCACTTGTAGAGCTGTGGGCGCATTCG	543
QY	184	atcaacgcctactgttaacatctgccacagctctcaatctggacacaactcttaacagcagaa	243
E1	544	ATCGATCGGTACATGAG	603
QY	244	aactccctctgcctacagctgcctctctatagctctcagagcgagcgctcgtgccaaactc	303
Dh	604	AAGGCGCATCTGTGCGCTGTCTACGCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT	663
QY	304	catctgtgagactctccagtaacagagccga---ggaatctactcgttgcacactctggcccaatcc	363
Dh	664	CTGCTTGCGGTGGAGAGAGAGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	723
QY	364	gtcagctctcggcctaaacagcctccgcctgagtgattctccactctctgtgcccatggatata	423
Dh	724	CGCTTCATACCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	783
QY	424	gtatcactctctcga	483
Dh	784	GTCATGTACTG	794

RESULT 15  
 US-08-406-855A-3  
 Sequence 3, Application US/08/106656A  
 Patent No. 5861309  
 ATYPICAL INFORMATION:  
 APPLICANT: Jonathan A. Bard et al.  
 TITLE OF INVENTION: DNA Encoding Human Alpha 1 Adrenomedullary Lipoprotein Lipase  
 TITLE OF INVENTION: Receptors and Uses Thereof  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent'n Release #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/406,855A  
 FILING DATE: 21-AUG-1995  
 CLASSIFICATION: A35  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 41317-A-PCT-US/JPW/KDB  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0526  
 INFORMATION FOR SEQ. ID NO.: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1736 base pairs  
 TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: N  
ANTI-SENSE: N

US-06-406-855A-3

Query Match	6.7%;	Score 58.2;	DB 2;	Length 1738;
Best Local Similarity	47.6%;	Pred. No. 1.5e-06;		
Matches 205;	Conservative	0;	Mismatches 223;	Indels 3; Gaps 1

OY	4	aacacattctgtgtgagccttaacgctgtggcagaacccgtgtgtgtgcacattatccgtaccca	63
OY	111		111
Db	364	AACTACTTCAATTCATCCCTGGCCATCGCCCACTGGCTGATGAACTTCAATGATGTTCCG	423
OY	64	ttgtgtctcatgtatgcataatttaacaaagggttgaaacctgagctatcgtcatgtttggaagc	123
OY	111		111
Db	424	TTCTTACCGCCGCCATAGAGGTGCTGGGCTACTGGGTGGCGGTGCATCTTTCTTCAATTC	483
OY	124	atgtgattcccgataggggcctcgagatgtgtgactgtgtcatatttaacataccggatctgac	183
OY	111		111
Db	484	TGGGTCAAGGTGTGGATGTCCTGATGTGTGTAACAGGCTGCATCTGTGAAGCTTGAAGCTATTCG	543
OY	184	atcaaccgctactgtttacatctgtgcacaagctctcaagtgtgcacaaactatcacagcgaay	243
OY	111		111
Db	544	ATGATACGCTACATATGGGGCTGCGCTACTCTCTGCATTAACCAATGATGATTTGCAAGG	603
OY	244	aacctccctctgtcaagtgatcctctcatalatgtctcctctaaaggcgagcgctcctgtcccaactc	303
OY	111		111
Db	604	AAAGGCATATTTGGTGGTCTTCTAGTGTGGCTGTCTGTCAACCTTTATTTGATATGAGGCT	663
OY	304	cgctcgtgagcactctccagtacgaaccca---gagattactctgtgaccttcgccaatcc	360
OY	111		111
Db	664	CTCTTTGGGTGGAAGAGAGCTGGGCAACCAATGACAAAGAAATGGTGGGATTAAGTAAGAA	723
OY	361	gtacagctcgcactatacacatccgctgtgtgtgttcttcacatcttctgtgtgtgtgtgtgt	420
OY	111		111
Db	724	CCCTCTATACCCCTCTTCTCGTGGTGTGGAGTCTTTTATATGCTTTGTAAGTCAATTCCTA	783
OY	421	gtatattctctg 431	
OY	111		
Db	784	GTCTATGTAAG 794	

Search completed: February 18, 2001, 20:20.11  
Job time: 12816 sec



Tue Feb 20 11:43:04 2001

us-09-226-046-5.rst

Page 1

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 18, 2001, 19:20:56 , Search time 1953.01 Seconds  
(without alignments)  
3277.123 Million cell updates/sec

Title: US-09-226-046-5  
Perfect score: 867  
Sequence: 1 ggaacacattctgtgtgtaq.....taaggtggaactccgtttaa 867

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: qb\_est1:  
2: qb\_est2:  
3: qb\_est3:  
4: qb\_est4:  
5: qb\_est5:  
6: qb\_est6:  
7: qb\_est7:  
8: qb\_est8:  
9: qb\_est9:  
10: qb\_est10:  
11: qb\_est11:  
12: qb\_est12:  
13: qb\_est13:  
14: qb\_est14:  
15: qb\_est15:  
16: qb\_est16:  
17: qb\_est17:  
18: qb\_est18:  
19: qb\_est19:  
20: qb\_est20:  
21: qb\_est21:  
22: qb\_est22:  
23: qb\_est23:  
24: qb\_est24:  
25: qb\_est25:  
26: qb\_est26:  
27: qb\_est27:  
28: qb\_est28:  
29: qb\_est29:  
30: qb\_est30:  
31: qb\_est31:  
32: qb\_est32:  
33: qb\_est33:  
34: qb\_est34:  
35: qb\_est35:  
36: qb\_est36:  
37: qb\_est37:  
38: qb\_est38:  
39: qb\_est39:  
40: qb\_est40:  
41: em\_estba:  
42: em\_estfm:  
43: em\_esthum1:  
44: em\_esthum2:  
45: em\_esthum3:  
46: em\_esthum4:  
47: em\_esthum5:  
48: em\_esthum6:  
49: em\_esthum7:  
50: em\_esthum8:  
51: em\_esthum9:  
52: em\_esthum10:  
53: em\_esthum11:  
54: em\_esthum12:  
55: em\_esthum13:  
56: em\_esthum14:  
57: em\_esthum15:  
58: em\_esthum16:  
59: em\_esthum17:  
60: em\_esthum18:  
61: em\_esthum19:  
62: em\_esthum20:  
63: em\_estin1:  
64: em\_estin2:  
65: em\_estin3:  
66: em\_estin4:  
67: em\_estov1:  
68: em\_estov2:  
69: em\_estp11:  
70: em\_estp12:  
71: em\_estp13:  
72: em\_estp14:  
73: em\_estp15:  
74: em\_estro1:  
75: em\_estro2:  
76: em\_estro3:  
77: em\_estro4:  
78: em\_estro5:  
79: em\_estro6:  
80: em\_estro7:  
81: em\_estro8:  
82: em\_estro9:  
83: em\_estro10:  
84: em\_estro11:  
85: em\_estro12:  
86: em\_estro13:  
87: qb\_est41:  
88: qb\_est42:  
89: qb\_est43:  
90: qb\_est44:  
91: qb\_est45:  
92: qb\_est46:  
93: qb\_est47:  
94: qb\_est48:  
95: qb\_est49:  
96: qb\_est50:  
97: qb\_est51:  
98: qb\_est52:  
99: qb\_est53:  
100: qb\_est54:  
101: qb\_est55:  
102: qb\_est56:  
103: qb\_est57:  
104: qb\_est58:  
105: qb\_est59:  
106: qb\_est60:  
107: qb\_est70:  
108: qb\_est71:  
109: qb\_est72:  
110: qb\_est73:  
111: qb\_est74:  
112: em\_esthum21:  
113: em\_esthum22:  
114: em\_esthum23:  
115: em\_estom1:  
116: em\_estom2:

```

117: em_estp16:
118: em_estp17:
119: em_estp18:
120: em_estp19:
121: em_estp20:
122: em_estp21:
123: em_estp22:
124: em_estp23:
125: em_estp24:
126: em_estp25:
127: em_estp26:
128: em_estp27:
129: em_estp28:
130: em_estp29:
131: em_estp30:
132: em_estp31:
133: em_estp32:
134: em_estp33:
135: em_estp34:
136: em_estp35:
137: em_estp36:
138: em_estp37:
139: em_estp38:
140: em_estp39:
141: em_estp40:
142: em_estp41:
143: em_estp42:
144: em_estp43:
145: em_estp44:
146: em_estp45:
147: em_estp46:
148: em_estp47:
149: em_estp48:
150: em_estp49:
151: em_estp50:
152: em_estp51:
153: em_estp52:
154: em_estp53:
155: em_estp54:
156: em_estp55:
157: em_estp56:
158: em_estp57:
159: em_estp58:
160: em_estp59:
161: em_estp60:
162: em_estp61:
163: em_estp62:
164: em_estp63:
165: em_estp64:
166: em_estp65:
167: em_estp66:
168: em_estp67:
169: em_estp68:
170: em_estp69:
171: em_estp70:
172: em_estp71:
173: em_estp72:
174: em_estp73:
175: em_estp74:
176: em_estp75:
177: em_estp76:
178: em_estp77:
179: em_estp78:
180: em_estp79:
181: em_estp80:
182: em_estp81:
183: em_estp82:
184: em_estp83:
185: em_estp84:
186: em_estp85:
187: em_estp86:
188: em_estp87:
189: em_estp88:

```

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed.  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	217.2	25.1	1101	193	CNS05KTS
2	190.4	22.0	938	192	CNS04CH1
3	153.2	17.7	618	193	PR0045009
4	139.6	16.1	1060	193	CNS05TUP
5	110.6	13.0	842	192	CNS04SOS
6	58.8	6.8	601	193	PR0045004
7	58.8	6.7	436	199	AC0610256
8	55.8	6.5	510	111	BE654347
9	55.8	6.5	510	111	BE654347
10	55.8	6.5	510	111	BE654347
11	54.5	6.3	666	97	AW666793
12	53.9	6.2	666	97	AW666793
13	53.4	6.2	866	191	CNS02RNL
14	53.4	6.2	866	191	CNS02RNL
15	53.4	6.2	866	191	CNS02RNL
16	52.4	6.0	310	5	AA296456
17	52.4	6.0	310	5	AA296456
18	52.4	6.0	310	5	AA296456
19	50.4	5.8	439	91	AM496772
20	50.4	5.8	439	91	AM496772
21	49.6	5.7	774	191	CNS02APC
22	49.6	5.7	934	192	CNS04S82
23	49.6	5.7	677	192	CNS04EAB
24	48.6	5.6	589	167	AC132344
25	47.8	5.5	460	24	AT759038
26	47.2	5.4	922	192	CNS04OER
27	47.2	5.4	922	192	CNS04OER
28	47.2	5.4	922	192	CNS04OER
29	47.2	5.4	922	192	CNS04OER
30	47.2	5.4	922	192	CNS04OER
31	46.8	5.4	421	105	BE426441
32	46.8	5.4	852	105	BE213339
33	46.8	5.4	885	105	BE213616
34	46.6	5.4	652	26	AT929343
35	46.2	5.3	386	20	AT457674
36	46.2	5.3	440	93	AW663056
37	46.2	5.3	538	28	AT728075
38	46.2	5.3	753	191	CNS02087
39	46.2	5.3	421	157	AC113645
40	46.2	5.3	720	168	AT196050
41	46.2	5.3	816	193	AA205847
42	45.8	5.2	1052	104	REF11770
43	45.8	5.2	611	172	AC435268
44	45.8	5.2	697	40	AW124038
45	45.2	5.2	976	105	BE213642

## ALIGNMENTS

RESULT 1  
 CNS05KTS/c 1101 bp DNA 26-MAY-2000  
 Tetradon nigriviridis genome survey sequence T3 end of clone  
 042601 of library A from Tetradon nigriviridis genome survey  
 sequence.  
 ACCESSION AT341929  
 VERSION AT341929.1 GI:8235687  
 KEYWORDS GSS: genome survey sequence.

[illegible][illegible]



Dy	686	GAAATTCTCATAACCATGTTTCGTGGTCTTCTTGCTCTTTGGCAATCGATCGAGGTCCACATCA	745
OY	578	aactcattgcccgcgcgcgtgcctcltgaccuccacagcatagtccctaggatccccagagt	637
Dd	746	AACtGAICGAGCTTGGGGGAGTGCACATGATGTCTGTCAGCTGAGGCCGCCGCCAATGCTTGAGGT	805
OY	638	ggctgtttgtgccaagttactacataggcgatttcga	674
Dd	806	CACCTTTTGTATGTAATACTTATTAAGCTACTTCAA	942
RESULT	6		
FP0045004/C			
LOCUS	FP0045004	601 bp	DNA GSS 22-OCT-1999
DEFINITION	Fugu rubripes GSS sequence, clone 199119PF11, genomic survey		
ACCESSION	AL132496.1	GI:6114442	
VERSION	ALI32496		
KEYWORDS	GSS; genome survey sequence		
SOURCE	Fugu rubripes.		
ORGANISM	Fugu rubripes		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;		
	Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorphia;		
	Tetraodoniformes; Tetraodonioidei; Tetraodontidae; Fugu.		
REFERENCE	1 (bases 1 to 601)		
AUTHORS	Elgar,G., Clark,M.S., Smith,S., Meek,S., Warner,S., Edwards,Y I K ,		
	Urnania,Y., Williams,G. and Brenner,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-Oct-1999) MRC Human Genome Mapping Project Resource		
	Centre, Hinxton, Cambridge, CB10 1SB, UK Email:		
	biohelp@hmp.mrc.ac.uk		
COMMENT	Vector: plasmid pUC19 KS		
	V-type: phagemid		
	PRIMER: KS		
DESCRIPTOR	One pass dye-terminator sequencing of cosmid cloned genomic		
	sequence.		
FEATURES			
source	Location/Qualifiers		
	1..601		
	/organism="Fugu rubripes"		
	/db_xref="taxon:31033"		
	/clone_lib="cosmid 199119"		
	/clone="199119PF11"		
BASE COUNT	83 a 121 c 174 g 133 t 90 others		
ORIGIN			
	Query Match 6.8%; Score 58.8; Db 193; Length 601;		
	Hest Local Similarity 62.8%; Freq No. 1.5e+05;		
	Matches 98; Conservative 0; Mismatches 57; Indels 1; Gaps 1;		
OY	713	aaaatctcagaagaatatcacagagaatttaagtcctgcctcgtgacagccagagattct	772
Dd	355	AACATCTCCGGCGGCGGAGACACANAGGCATACCTGNTGTGGTATGAAATGATGATCTNN	296
OY	773	tgtgtagacagc-tctaacgacagctgagccgataggttaataggaacacctcacatcata	831
Dd	299	NTCAGAGCANAGTTCMAAGACGCGCGGACAGAGGTANCANAGCAAACCTCGCGGCTATG	236
OY	832	accacaataatgtagtaaagtgactccgttaa	867
Dd	235	ACCACAACACACACAGGTCAAGTAGTGGACTGGTCTGA	200
RESULT	7		
AO610256			
LOCUS	AO610256	436 bp	DNA GSS 15-JUN-1999
DEFINITION	HS-5094_A1.H03.SP6E.RPci-11 Human Male BAC Library Homo sapiens		
ACCESSION	AO610256		
VERSION	AO610256.1	GI:5071532	
KEYWORDS	GSS.		
SOURCE	human.		





## RESULT 10

DEFINITION	ES2778867	MATR.	rosenquercus	MAG1	HOMO	Sapiens	ELINE1	ENSEMBL	ENSEMBL
ACCESSION	AW966793								
VERSION	AW966793.1	GI:	8156629						

rosaguanines, MAGI Homo sapiens cDNA, mRNA sequences



```

De      367 TTTTCTACCAATTTCCTGCTGTGGAAAG
RESULT  13
CNS02RNL          CNS02PNI           866 bp      DNA          GSS          14 MAY-2000
LOCUS         Tetraodon nigroviridis genome survey sequence PUC-ori end of clone
DEFINITION    160024 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION     AL210810
KEYWORDS      GSS: genome survey sequence.
SOURCE        Tetraodon nigroviridis.
ORGANISM      Tetraodon nigroviridis.
REFERENCE     Poest-Crollius,H., Jallouin,C., Essilva,G., Fizames,G., Fisher,A.,
AUTHORS       Bouneau,L., Billault,A., Queller,F., Saurin,W., Bernot,A. and
              Weissbach,J.
TITLE         Characterization and repeat analysis of the compact genome of the
              freshwater puterfish Tetraodon nigroviridis
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 866)
AUTHORS       Poest-Crollius,H., Jallouin,C., Essilva,G., Bouneau,L., Fisher,A.,
              Bernot,A., Fizames,G., Winkler,P., Brottier,P., Queller,F.,
              Saurin,W. and Weissbach,J.
TITLE         Human gene number estimate provided by genome wide analysis using
              Tetraodon nigroviridis DNA sequence
JOURNAL       Unpublished
REFERENCE     3 (bases 1 to 866)
AUTHORS       Genoscope.
TITLE         Direct Submission
JOURNAL       Submitted (12-Apr-2000) to the EMBL/GenBank/DBJ databases
COMMENT       This sequence is a single read and was generated as part of a large
              scale clone-end sequencing project of the Tetraodon nigroviridis
              genome. For more information, please take a look at
              http://www.genoscope.cns.fr/Tetraodon.
FEATURES
             source            1..866
                               /organism="Tetraodon nigroviridis"
                               /db_xref="taxon:99883"
                               /clone="160024"
                               /clone_lib="G"
                               /note="Genoscope sequence ID : CQA016BHN12spi-end"
BASE COUNT   155 a      28 c      22 g      15 t      13 other
ORIGIN
Query Match      6.2% Score 53.4; DB 191; Length 866;
Best Local Similarity 47.4%; E-val: No. 0.00051;
Matches 175; Conservative 5; Mismatches 186; Indels 3; Gaps 1
1 ggaacaacattctgtggttgaagccttagcggttggaacacctgtgtggccacttatccgttag 60
|||||
212 GGMSAGCATCTACATTTGGAAACTTGCGCTTTCCCTGCACCTGCACTTCCTGCGTAGATTACCG 272
|||
61 ccgttgtctgtatgcgcgatatttaacaagggttgaaccctggcatctgtcacctgccaa 120
|||||
273 CTGTGTAATGCTGTGAACAAGGAGGATGAGGATGATGATGATGATGATGATGATGATGAT 332
|||||
121 gtcaatggatttcctgaatggagcctggagcgttcattgtgtccatatcaaatcacaggatc 180
|||||
333 ATGAGCACAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 392
|||||
181 ggcataaacgcctacatcttacatctgcacacacatcctaagtggcacaacaactgacagcagg 240
|||||
393 AATTTTAAATGCTAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 452

```

[illegible]



GenCore version 4.5  
Copyright (C) 1993 - 2000 CompuGen Ltd

OM protein - protein search, using sw model

Run on: February 19, 2001, 16:45:08 Search time 72.17 Seconds  
(without alignments)  
136 453 Million cell updates/sec

Title: US-09-226-046-6

Perfect score: 1514  
Sequence: 1 GNIFVSLAVADLVVAIPY... VKKPSPLTNNVAVLSV 285

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database: 1. A\_Geneseq\_16.\*  
2. /cgn2\_2/gcdata/geneseq/geneseq/AA1981.DAT.\*  
3. /cgn2\_2/gcdata/geneseq/geneseq/AA1982.DAT.\*  
4. /cgn2\_2/gcdata/geneseq/geneseq/AA1983.DAT.\*  
5. /cgn2\_2/gcdata/geneseq/geneseq/AA1984.DAT.\*  
6. /cgn2\_2/gcdata/geneseq/geneseq/AA1985.DAT.\*  
7. /cgn2\_2/gcdata/geneseq/geneseq/AA1986.DAT.\*  
8. /cgn2\_2/gcdata/geneseq/geneseq/AA1987.DAT.\*  
9. /cgn2\_2/gcdata/geneseq/geneseq/AA1988.DAT.\*  
10. /cgn2\_2/gcdata/geneseq/geneseq/AA1989.DAT.\*  
11. /cgn2\_2/gcdata/geneseq/geneseq/AA1990.DAT.\*  
12. /cgn2\_2/gcdata/geneseq/geneseq/AA1991.DAT.\*  
13. /cgn2\_2/gcdata/geneseq/geneseq/AA1992.DAT.\*  
14. /cgn2\_2/gcdata/geneseq/geneseq/AA1993.DAT.\*  
15. /cgn2\_2/gcdata/geneseq/geneseq/AA1994.DAT.\*  
16. /cgn2\_2/gcdata/geneseq/geneseq/AA1995.DAT.\*  
17. /cgn2\_2/gcdata/geneseq/geneseq/AA1996.DAT.\*  
18. /cgn2\_2/gcdata/geneseq/geneseq/AA1997.DAT.\*  
19. /cgn2\_2/gcdata/geneseq/geneseq/AA1998.DAT.\*  
20. /cgn2\_2/gcdata/geneseq/geneseq/AA1999.DAT.\*  
21. /cgn2\_2/gcdata/geneseq/geneseq/AA2000.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1514	100.0	288	17	High-affinity mela
2	1443.5	95.3	350	17	High-affinity mela
3	1443.5	95.3	350	18	Melatonin receptor
4	1436.5	94.9	350	20	Human melatonin re
5	1308.5	86.4	353	19	Mouse melatonin 1a
6	1292.5	85.4	353	17	High-affinity mela
7	1241.5	82.0	354	18	High-affinity mela
8	1059.5	70.0	354	17	Xenopus melatonin
9	1059.5	70.0	420	18	Xenopus melatonin
10	1049.5	69.3	354	17	High-affinity mela
11	889.5	58.8	362	17	High-affinity mela
12	285	18.8	349	16	Galanin receptor.

13	285	18.8	349	17	R95070	Human galanin rece
14	281	18.6	346	20	Y45129	Rat galanin recept
15	279	18.4	348	17	R95069	Mouse pancreas bet
16	279	18.4	348	17	R93229	Mouse pancreas G-P
17	277.5	18.3	408	21	Y76882	Human NPY-Y7 recep
18	277.5	18.3	420	20	W81358	Human 7-transmembr
19	277.5	18.3	420	21	Y79375	Human neuropeptide F
20	277.5	18.3	417	21	Y79377	Human neuropeptide F
21	267.5	17.5	428	21	Y56887	Human N5 receptor
22	264.5	17.5	401	21	Y68880	Rat neuropeptide F
23	264.5	17.5	432	21	Y79373	A murine mu-opioid
24	263.5	17.4	430	21	Y79376	Kat neuropeptide F
25	261.5	17.3	391	21	Y68886	A murine neuropeptide
26	260.5	17.2	432	21	Y68886	A murine mu-opioid
27	260	17.2	356	15	W65181	Rat B5 receptor po
28	260	17.2	398	16	R76781	Murine mu subtype
29	260	17.2	398	16	R71564	Rat mu opiate rece
30	258.5	17.1	359	21	Y68878	A murine mu-opioid
31	258.5	17.1	390	21	Y68885	A murine mu-opioid
32	258.5	17.1	392	21	Y68885	A murine mu-opioid
33	258.5	17.1	392	19	W44937	Mouse mu opiate re
34	258.5	17.1	399	21	Y68881	A murine mu-opioid
35	258.5	17.1	409	21	Y68887	A murine mu-opioid
36	258.5	17.1	438	21	Y68877	A murine mu-opioid
37	258.5	17.1	444	21	Y68888	A murine mu-opioid
38	258	17.0	370	17	R91218	Human pituitary G-
39	258	17.0	370	18	W31379	Human G-protein-co
40	258	17.0	370	20	W57221	Human pituitary-de
41	258	17.0	370	20	W57181	Human G-protein-co
42	258	17.0	380	18	W27510	Consensus human by
43	257.5	17.0	398	21	Y68889	A murine mu-opioid
44	257.5	17.0	400	15	P76780	Human mu opiate re
45	257.5	17.0	400	16	R71966	Human mu opiate re

## ALIGNMENTS

RESULT 1	
R88411	
16-AUG-1996 (first entry)	
High-affinity melatonin-1a receptor fragment.	
Melatonin-1a receptor, human, G-protein-coupled receptor;	
cytochrome-c family home binding site; antibody;	
melatonin receptor-agonist; melatonin receptor-antagonist;	
KW circadian rhythm disorder; jet lag; day-night cycle disorder;	
KW ovulation; reproductive cycle; animal breeding; puberty;	
KW transgenic animal; drug screening.	
XX Homo sapiens.	
XX Location/Qualifiers	
XX Key	
XX Domain	
XX FT	1..2
XX FT	/note= "Intracellular loop fragment"
XX FT	1..6
XX FT	/note= "Conserved melatonin receptor motif"
XX FT	3..27
XX FT	/note= "Transmembrane region-II"
XX FT	28..41
XX FT	/note= "Extracellular loop"
XX FT	42..60
XX FT	/note= "Transmembrane region-III"
XX FT	61..85
XX FT	/note= "Intracellular loop"
XX FT	66..71
XX FT	/note= "Putative cytochrome-c family home binding site"
XX FT	72..104
XX FT	Domain



PD 28-DEC-1995.  
 XX 07-JUN-1995: 95WC-0507360  
 XX 06-JUN-1995: 95US-0319887  
 PR 17-JUN-1994: 94US-0261857  
 PR 07-OCT-1994: 94US-0319887  
 XX (MASS-) MASSACHUSETTS GEN HOSPITAL.  
 XX Reprint SM:  
 DP WPI: 1996-058368/06.  
 DR N-PSDB: T09950.  
 XX DNA encoding high affinity melatonin receptor cDNA used to identify  
 PT receptor agonists or antagonists e.g. for regulating circadian  
 PT rhythm disorders or reproductive cycles  
 XX  
 PS Claim 8: Fig 5: 115pp: English.  
 XX The sequence represents a human high-affinity melatonin-1a  
 CC receptor, which is a membrane protein, coupled to guanine  
 CC nucleotide binding proteins (G-proteins), with 7 hydrophobic  
 CC putative transmembrane domains. A partial sequence is given in  
 CC R88411. The N-terminus contains 2 consensus N-glycosylation sites,  
 CC compared to 1 site in the Xenopus receptor (R88409), and the  
 CC C-terminal tail is 65 amino acids shorter. Receptor fragments which  
 CC interact with melatonin, or specific antibodies, may be used as  
 CC receptor-agonists or receptor-antagonists. Agonists may be used  
 CC in therapy of circadian rhythm disorders such as jet-lag or  
 CC day-night cycle disorders, to control ovulation, or in alteration  
 CC of reproductive cycles in seasonally breeding animals. Antagonists  
 CC may be used to control the initiation or timing of puberty in  
 CC humans. The receptor gene may also be expressed in a transgenic  
 CC animal for use as a model system to screen agonists and antagonists.  
 CC  
 XX Sequence 350 AA.  
 SQ  
 Query Match 95.3%; Score 1443.5; DB 17; Length 350;  
 Best Local Similarity 96.9%, Pred. No. 2,2e-152;  
 Matches 280; Conservative 1; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 GNIFVSLAVADLVVAIPYPLVMSIFNNGMNIGYHCQVSGFLMGISVIGSIFNITGI 60  
 DB 62 GNIFVSLAVADLVVAIPYPLVMSIFNNGMNIGYHCQVSGFLMGISVIGSIFNITGI 121  
 QY 61 AINPCYICHSKCKDKLYSSKNSLCYVLLWLT-AAVLPMLRGTLQYEPRIYSCFPAQ 119  
 DB 122 AINPCYICHSKCKDKLYSSKNSLCYVLLWLT-AAVLPMLRGTLQYEPRIYSCFPAQ 181  
 QY 120 SVSSAYTIAVAVFHELVPMIIVIFCYLRIMWILVQVOPVKKPKPKPKPKPKPKPKPK 179  
 DB 182 SVSSAYTIAVAVFHELVPMIIVIFCYLRIMWILVQVOPVKKPKPKPKPKPKPKPKPK 241  
 QY 130 VYFVFLAICWAPLNTIGLAVASDPASWPRIPKPLFVASYMAVFNCSLAIISGYWNQN 239  
 DB 242 VYFVFLAICWAPLNTIGLAVASDPASWPRIPKPLFVASYMAVFNCSLAIISGYWNQN 301  
 QY 240 FPKYEPFITVSLTAVAFVFDSSNDVADRVKPKPSPLMTNNNVKVDV 288  
 DB 302 FPKYEPFITVSLTAVAFVFDSSNDVADRVKPKPSPLMTNNNVKVDV 350  
 RESULT 3  
 W15786  
 ID W15786 standard: Protein: 350 AA.  
 XX  
 AC W15786:  
 XX  
 DT 23-JUN-1997 (first entry)  
 XX

DE Melatonin receptor protein.  
 XX  
 KW Melatonin receptor protein; human; chinese hamster ovary cell; CHO cell;  
 KW jet lag; sleeplessness; seasonal melancholia; Alzheimer's disease;  
 KW dementia; cerebral thrombosis; high blood pressure; cancer; melancholia;  
 KW ovulation regulator; neurosis; mental confusion; glaucoma; therapy.  
 XX  
 OS Homo sapiens.  
 XX JP09084581-A.  
 PN  
 XX 31-MAR-1997.  
 PD  
 XX 26-SEP-1995. 95JP-0248177.  
 PF  
 XX 26-SEP-1995. 95JP-0248177.  
 PR  
 XX (TAKEDA) TAKEDA CHEM IND LTD.  
 PA  
 XX WPI: 1997-252999/23.  
 DR N-PSDB: T60593.  
 DR  
 XX Claim 2; Page 16; 21pp; Japanese.  
 XX This sequence represents the human melatonin receptor protein. The DNA  
 CC encoding this sequence is used in an expression vector designated  
 CC pAKKO-hm187. The expression vector is used to produce the chinese  
 CC hamster ovary (CHO) cells of the invention. The CHO cells express the  
 CC human melatonin receptor protein, and can be used to identify compounds  
 CC (such as agonists and antagonists) having affinity to the receptor. The  
 CC CHO cells can also be used to produce the receptor. The melatonin  
 CC receptor agonist can be used as an agent for preventing or treating jet  
 CC lag, sleeplessness, seasonal melancholia, Alzheimer's disease, dementia,  
 CC blood pressure, cancer, and glaucoma. The melatonin receptor can also be  
 CC used as an ovulation regulator. The melatonin receptor antagonist can be  
 CC used as an agent for preventing or treating melancholia, neurosis, or  
 CC mental confusion.  
 CC  
 XX Sequence 350 AA;  
 SQ  
 Query Match 95.3%; Score 1443.5; DB 18; Length 350;  
 Best Local Similarity 96.9%, Pred. No. 2,2e-152;  
 Matches 280; Conservative 1; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 GNIFVSLAVADLVVAIPYPLVMSIFNNGMNIGYHCQVSGFLMGISVIGSIFNITGI 60  
 DB 62 GNIFVSLAVADLVVAIPYPLVMSIFNNGMNIGYHCQVSGFLMGISVIGSIFNITGI 121  
 QY 61 AINPCYICHSKCKDKLYSSKNSLCYVLLWLT-AAVLPMLRGTLQYEPRIYSCFPAQ 119  
 DB 122 AINPCYICHSKCKDKLYSSKNSLCYVLLWLT-AAVLPMLRGTLQYEPRIYSCFPAQ 181  
 QY 120 SVSSAYTIAVAVFHELVPMIIVIFCYLRIMWILVQVOPVKKPKPKPKPKPKPKPKPK 179  
 DB 182 SVSSAYTIAVAVFHELVPMIIVIFCYLRIMWILVQVOPVKKPKPKPKPKPKPKPKPK 241  
 QY 180 VYFVFLAICWAPLNTIGLAVASDPASWPRIPKPLFVASYMAVFNCSLAIISGYWNQN 239  
 DB 242 VYFVFLAICWAPLNTIGLAVASDPASWPRIPKPLFVASYMAVFNCSLAIISGYWNQN 301  
 QY 240 FPKYEPFITVSLTAVAFVFDSSNDVADRVKPKPSPLMTNNNVKVDV 288  
 DB 302 FPKYEPFITVSLTAVAFVFDSSNDVADRVKPKPSPLMTNNNVKVDV 350  
 RESULT 4  
 W94761

10 W94761 standard; Protein: 350 AA.  
 AC W94761;  
 XX  
 XX 28-APR-1999 (first entry)  
 DT  
 XX Human melatonin receptor protein mel-1a.  
 DE  
 XX Melatonin receptor; mel-1a; human; screening; hormone  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Misc-difference 249  
 FT /note= "encoded by ART"  
 FT Misc-difference 274  
 FT /note= "encoded by SAG"  
 FT  
 FT  
 PN EP892046-A2.  
 XX  
 XX 20-JAN-1999.  
 PD  
 XX 19-JUN-1998; 98EP-0111352.  
 PE  
 XX 19-JUN-1997; 97JP-0180537.  
 PR  
 XX (JCRP-) JCR PHARM CO LTD.  
 PA  
 XX Koda J. Shirota H. Yokoyama T.  
 PI  
 XX WPI: 1999-083563/08.  
 DR N PSDR: X05747  
 XX  
 XX New melatonin-receptor expression cells - useful for screening for  
 PT human melatonin receptor proteins and agonists and antagonists  
 FT  
 FT Examples: Fig 2; 24pp; English  
 XX  
 XX This represents a human melatonin receptor mel-1a. The invention  
 CC provides materials for screening for a substance showing affinity for a  
 CC melatonin receptor protein, which comprises an animal cell containing an  
 CC expression plasmid for the gene encoding a human melatonin receptor  
 CC protein. The cells are useful for screening for human melatonin receptor  
 CC proteins and its agonist or antagonist e.g. hormones and synthetic  
 CC compounds, by measuring changes in metabolic activity. The recombinant  
 CC human melatonin receptor protein is useful as it has the same activity as  
 CC natural human melatonin receptor protein. The new screening method is  
 CC better than prior art radioimmunoassay techniques at quantitatively  
 CC determining melatonin, which uses antibodies produced by linking  
 CC melatonin to a carrier.  
 CC  
 CC Sequence: 450 AA.  
 XX  
 XX Query Match 94.9%; Score 1436.5; DR 20; Length 350;  
 XX Post Local Similarity 96.2%; Pred. No. 136-151;  
 XX Matches 279; Conservative 2; Mismatches 8; Indels 1; Gaps 1;  
 XX  
 XX 1 GRTFVSLAVADLVAVIYPPYPLVLMKIFNNQNLSTLHCVSGFLMSLVISINIRI 60  
 DB  
 XX 62 qnlvslavadvavaiyppylvmlsmnawtqyhcyqsgflmgslvisislnl 121  
 XX  
 XX 61 AINRYCYCHSLKGRKLYSSKNSLCVLLMLLT-AAVPLNLPKGLQVEPRYSCTFAQ 119  
 DB  
 XX 122 ainyrychslkgrklyssksnslcvllmltlaavplnlpkglqveprysctf 181  
 XX  
 XX 120 SVSSAVTAVVVFHPLVPMIVIFCYLRILWLVLQVQVKKDPKPKLKPHDFPNTWF 179  
 DB  
 XX 182 svssavtlavvvfhlvpmivifcyllrilmvlvqvgvkkdkpkdkpqrdfntwtf 241  
 XX  
 XX 180 VVWFVLAIAIMALNLSGLVSNVSNVSNVSNVSNVSNVSNVSNVSNVSNVSNVSN 239  
 DB  
 XX 242 vvfwvllaiaimalnls glvsnvsnvsnvsnvsnvsnvsnvsnvsnvsnvsnvsn 301

XX 240 FPEEPPITVITAPVFEVSSNDVADPKPKPSPLMNNNVAVDSV 288  
 DB  
 XX 302 fpeepptvitytapvfevssndvadpkpkpsplmnnnvavdsv 350  
 XX  
 XX RESULT 5  
 XX W23958  
 XX W23958 standard; Protein: 353 AA.  
 AC W23958;  
 XX  
 XX 06-JUL-1998 (first entry)  
 DT  
 XX Mouse melatonin 1a receptor.  
 DE  
 XX Melatonin 1a receptor. Mel-1a gene. Circadian rhythm; puberty;  
 KW reproductive cycle; jet lag; mouse; G-protein coupled receptor.  
 XX  
 XX Mus musculus.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 4..6  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 10..12  
 FT /note= "Asn is N-glycosylated"  
 FT Region 31..35  
 FT /label= I  
 FT /note= "Transmembrane region I"  
 FT Region 66..91  
 FT /label= II  
 FT /note= "Transmembrane region II"  
 FT Region 106..124  
 FT /label= III  
 FT /note= "Transmembrane region III"  
 FT Modified-site 135..137  
 FT /note= "Ser is O-phosphorylated"  
 FT Modified-site 141..145  
 FT /note= "Ser is O-phosphorylated"  
 FT Region 150..169  
 FT /label= IV  
 FT /note= "Transmembrane region IV"  
 FT Region 192..218  
 FT /label= V  
 FT /note= "Transmembrane region V"  
 FT Region 242..266  
 FT /label= VI  
 FT /note= "Transmembrane region VI"  
 FT Region 278..298  
 FT /label= VII  
 FT /note= "Transmembrane region VII"  
 XX  
 XX W09803549-A1.  
 PN  
 XX 29-JAN-1998.  
 PD  
 XX 17-JUL-1997; 97WO-US12526.  
 PE  
 XX 18-JUL-1996; 96US-0022185.  
 PR  
 XX (GEHO) GEN HOSPITAL CORP.  
 PA  
 XX Peppert SM;  
 PI  
 XX WPI: 1998-120701/11.  
 DR N-PSDB; V04644.  
 XX  
 XX Nucleic acid comprising melatonin 1a receptor promoter and reporter  
 PT gene - used to transform cells for screening for agents that alter  
 PT transcription from promoter, e.g. for correcting circadian rhythm  
 PT disorders or controlling reproduction in animals  
 XX  
 XX Description: Page 32; 46pp; English.



XX This protein comprises the mouse melatonin 1a (Mella) receptor, a  
 CC G-protein coupled receptor that specifically binds melatonin and  
 CC signals the melatonin-mediated cascade of biological events. A  
 CC claimed nucleic acid (1) comprises a functional melatonin 1a  
 CC receptor gene promoter (see V04644) linked to a reporter gene.  
 CC Cells containing (1) are used to screen compounds (A) for ability  
 CC to alter transcription from the promoter (claimed). (A) that are  
 CC activators are useful for treating circadian rhythm disorders in  
 CC humans (e.g. jet lag, sleep-wake disturbances in the blind or  
 CC regulation of ovarian cyclicity) and for control of the  
 CC reproductive cycle in seasonally breeding animals, while those that  
 CC are inhibitors are used to control initiation and timing of puberty  
 CC in humans. Screening for (A) can now be done in cultures of  
 CC transformed cells which do not naturally express the receptor (which  
 CC is naturally localised to a few specific sites in the central nervous  
 CC system).  
 CC  
 CC Sequence 353 AA:  
 SQ  
 Query Match 86.4%; Score 1308.5; DB 19; Length 353;  
 Best Local Similarity 84.4%; Pred. No. 2,36-137; Indels 1; Gaps 1;  
 Matches 244; Conservative 25; Mismatches 19;  
 1 GNIFVVSLLAVADLVVAIVYPPYLMSIFNNNGNLCYHCOVSGFLMGLSVIGSIFNTGI 60  
 65 gnlfvvsllavadvlvvaivypylmstfnnngnlylhcqvsaflmgslvsgsifntgl 124  
 QY 61 AINPVCYICHSKCKDKLYSKNSLCYVLLIMLT-AAVLPNLRPTLOVEPRIVSCTPAQ 119  
 125 amnrvcyichskckdklysknslcyvllimltaimpnlqglaydrivsccttg 184  
 QY 120 SVSSAVTIAVAVVHFPLVPMITVFCYLRIMVILVQVPPVPRPKPKPHDPFNFVTMF 179  
 185 svssavtiaavvvhfplvpmivtfcyllrilmvilyvrrivkphdkpkpkqdfnfvtmf 244  
 Db 180 VVFLPAICWAPLNFITGLAVASDPASMPRIPEMLFVASYVAAYFNSCINAIISQYMNQ 239  
 245 vvflfaicwaplnlfiglvaasdpasmpripewlfvasyylayfnsclnaiiyllnqn 304  
 QY 240 FPKYEPPIIVSLTAVPFFVDSNDVADRVKRPSPFLMTNNNVKVDV 288  
 305 frkeykpiivslctakmfvessneeadkikcspplipnnnlikvdsv 353  
 Db  
 RESULT 6  
 R88413  
 ID R88413 standard: Protein: 353 AA.  
 XX  
 AC R88413:  
 XX  
 DT 16-AUG-1996 (first entry)  
 DE High-affinity melatonin-1a receptor.  
 XX  
 KW Melatonin-1a receptor; mouse; G-protein-coupled receptor;  
 KW melatonin receptor-agonist; melatonin receptor-antagonist;  
 KW circadian rhythm disorder; jet-lag; day-night cycle disorder;  
 KW ovulation; reproductive cycle; animal breeding; puberty;  
 KW antibody; transgenic animal; drug screening.  
 XX  
 CS Mus musculus.  
 XX  
 FN W09535320-A1.  
 XX  
 PD 28-DEC-1995.  
 XX  
 PF 07-JUN-1995; 95W0-US07350.  
 XX  
 PR 06-JUN-1995; 95US-0319887.  
 PR 17-JUN-1994; 94US-0251957.  
 PR 07-OCT-1994; 94US-0319887.

XX (MARS-) MASSACHUSETTS GEN HOSPITAL.  
 PA  
 XX Reppert SM;  
 XX  
 XX WPI; 1996-058368/06.  
 DR N-PSDB; T09951.  
 XX  
 PS DNA encoding high affinity melatonin receptor one - used to identify  
 PT receptor agonists or antagonists e.g. for regulating circadian  
 PT rhythm disorders or reproductive cycles  
 XX  
 PS Claim 9; Fig 3; 115pp; English.  
 XX  
 CC The sequence represents a mouse high-affinity melatonin-1a receptor,  
 CC which is a membrane protein, coupled to guanine nucleotide binding  
 CC proteins (G-proteins). Receptor fragments which interact with  
 CC melatonin, or specific antibodies, may be used as receptor-agonists  
 CC or receptor-antagonists. Agonists may be used in therapy of  
 CC circadian rhythm disorders such as jet lag or day-night cycle  
 CC disorders, to control ovulation, or in alteration of reproductive  
 CC cycles in seasonally breeding animals. Antagonists may be used to  
 CC control the initiation or timing of puberty in humans. The  
 CC receptor gene may also be expressed in a transgenic animal for use  
 CC as a model system to screen agonists and antagonists.  
 CC  
 CC Sequence 353 AA:  
 SQ  
 Query Match 85.4%; Score 1292.5; DB 17; Length 353;  
 Best Local Similarity 83.7%; Pred. No. 1,4e-135;  
 Matches 242; Conservative 24; Mismatches 22; Indels 1; Gaps 1;  
 1 GNIFVVSLLAVADLVVAIVYPPYLMSIFNNNGNLCYHCOVSGFLMGLSVIGSIFNTGI 60  
 65 gnlfvvsllavadvlvvaivypylmstfnnngnlylhcqvsaflmgslvsgsifntgl 124  
 QY 61 AINPVCYICHSKCKDKLYSKNSLCYVLLIMLT-AAVLPNLRPTLOVEPRIVSCTPAQ 119  
 125 amnrvcyichskckdklysknslcyvllimltaimpnlqglaydrivsccttg 184  
 QY 120 SVSSAVTIAVAVVHFPLVPMITVFCYLRIMVILVQVPPVPRPKPKPHDPFNFVTMF 179  
 185 svssavtiaavvvhfplvpmivtfcyllrilmvilyvrrivkphdkpkpkqdfnfvtmf 244  
 Db 180 VVFLPAICWAPLNFITGLAVASDPASMPRIPEMLFVASYVAAYFNSCINAIISQYMNQ 239  
 245 vvflfaicwaplnlfiglvaasdpasmpripewlfvasyylayfnsclnaiiyllnqn 304  
 QY 240 FPKYEPPIIVSLTAVPFFVDSNDVADRVKRPSPFLMTNNNVKVDV 288  
 305 frkeykpiivslctakmfvessneeadkikcspplipnnnlikvdsv 353  
 Db  
 RESULT 7  
 R88410  
 ID R88410 standard: Protein: 366 AA.  
 XX  
 AC R88410:  
 XX  
 DT 15-AUG-1996 (first entry)  
 DE High-affinity melatonin-1a receptor.  
 XX  
 KW Melatonin-1a receptor; sheep; G-protein-coupled receptor;  
 KW cytochrome-c family heme binding site; melatonin receptor-agonist;  
 KW melatonin receptor-antagonist; circadian rhythm disorder; jet-lag;  
 KW day-night cycle disorder; ovulation; reproductive cycle; antibody;  
 KW animal breeding; puberty; transgenic animal; drug screening.  
 XX  
 CS Ovis aries.  
 XX  
 OS  
 Key Location/Qualifiers

FT Domain 1..43 /note- "Extracellular domain"  
 FT Modified-site 16..18 /note- "N-glycosylation site"  
 FT Modified-site 23..25 /note- "N-glycosylation site"  
 FT Domain 44..68 /note- "Transmembrane region-1"  
 FT Domain 69..79 /note- "Intracellular loop"  
 FT Region 78..83 /note- "Conserved melatonin receptor motif"  
 FT Domain 80..104 /note- "Transmembrane region-II"  
 FT Domain 105..118 /note- "Extracellular loop"  
 FT Domain 119..137 /note- "Transmembrane region-III"  
 FT Domain 138..162 /note- "Intracellular loop"  
 FT Region 143..148 /note- "Putative cytochrome-c family heme binding site"  
 FT Domain 163..182 /note- "Transmembrane region-IV"  
 FT Domain 183..204 /note- "Extracellular loop"  
 FT Domain 205..231 /note- "Transmembrane region-V"  
 FT Domain 232..254 /note- "Intracellular loop"  
 FT Domain 255..279 /note- "Transmembrane region-VI"  
 FT Domain 280..290 /note- "Extracellular loop"  
 FT Domain 291..312 /note- "Transmembrane region-VII"  
 FT Region 307..311 /note- "Conserved melatonin receptor-1a motif"  
 FT Domain 313..366 /note- "Intracellular domain"  
 FN W 09535320 A1  
 XX 28-DEC-1995.  
 XX 07-JUN-1995: 95WO-0807360.  
 XX 06-JUN-1995: 95US-0319887.  
 XX 17-JUN-1994: 94US-0261857.  
 XX 07-OCT-1994: 94US-0319887.  
 XX (MARS-) MASSACHUSETTS GEN HOSPITAL.  
 XX Report SM:  
 XX WPI: 1996-058368700.  
 XX N-PSDB: T09946.  
 PT DNA encoding high affinity melatonin receptor gene - used to identify  
 PT receptor agonists or antagonists e.g. for regulating circadian  
 PT rhythm disorders or reproductive cycles  
 PS Claim 6: Fig 2: 115pp: English.  
 XX The sequence represents a sheep high-affinity melatonin-1a  
 XX receptor, which is a membrane protein, coupled to guanine  
 XX nucleotide binding proteins (G-proteins), with 7 hydrophobic  
 XX putative transmembrane domains. Receptor fragments which interact  
 XX with melatonin, or specific antibodies, may be used as  
 XX receptor-agonists or receptor-antagonists. Agonists may be used in  
 XX therapy of circadian rhythm disorders such as jet-lag or day-night  
 XX cycle disorders, to control ovulation or in alteration of  
 XX reproductive cycles in seasonally breeding animals. Antagonists

CC may be used to control the initiation or timing of puberty in  
 CC humans. The receptor gene may also be expressed in a transgenic  
 CC animal for use as a model system to screen agonists and antagonists.  
 XX  
 SO Sequence 366 AA:  
 Query Match 82.0%; Score 1241.5; DB 17; Length 366;  
 Best Local Similarity 80.6%; Pred. No. 6,8e-130;  
 Matches 223; Conservative 25; Mismatches 30; Indels 1; Gaps 11  
 QY 1 GNFFVSLAVADLVVAIPYPIVMSIFNNGNLGYHCOVSGFLMGSLVIGSIFNIGI 60  
 DB 78 GNFFVSLAVADLVVAIPYPIVMSIFNNGNLGYHCOVSGFLMGSLVIGSIFNIGI 137  
 QY 61 AINRYVYCHSLKQDKRYSSKSLVYLWLMLT-AAVLPNLYKGLQYPPRISCFAG 119  
 DB 138 AINRYVYCHSLKQDKRYSSKSLVYLWLMLT-AAVLPNLYKGLQYPPRISCFAG 197  
 QY 120 SVSSARVIAVVEHFLVLMVLVLYPLIMLVLYVWGVKPKPKPKPKPKPKPKPK 179  
 DB 126 SVSSARVIAVVEHFLVLMVLVLYPLIMLVLYVWGVKPKPKPKPKPKPKPKPK 257  
 QY 120 VVEVLEATVWATNFGSLAVASFGASVFPFEMLEFASVYVAEVSCLNAISGVWGN 239  
 DB 258 VVEVLEATVWATNFGSLAVASFGASVFPFEMLEFASVYVAEVSCLNAISGVWGN 317  
 QY 240 FPKRPPIVSLTAVPFVDSNDVADPKPKPSPLMNNVKKVDSV 288  
 DB 240 FPKRPPIVSLTAVPFVDSNDVADPKPKPSPLMNNVKKVDSV 366  
 RESULT 8  
 W25926 standard: Protein: 354 AA.  
 AC W25926;  
 XX 10-NOV-1997 (first entry)  
 DE Xenopus laevis.  
 XX Allele: Xenopus laevis; melatonin; receptor; untranslated region; PCR;  
 KW mRNA; half-life; skin; amplification; primer; polymerase chain reaction;  
 KW transmembrane domain; cellular signaling; inhibition; adenylyl cyclase;  
 KW modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase.  
 XX Xenopus laevis.  
 OS Location/Qualifiers  
 FH Key 1..32 /note- "Extracellular N-terminal domain"  
 FT Domain 33..56 /note- "Transmembrane domain 1"  
 FT Domain 57..68 /note- "Intracellular domain 1"  
 FT Domain 69..92 /note- "Transmembrane domain 2"  
 FT Domain 93..107 /note- "Extracellular domain 2"  
 FT Domain 108..125 /note- "Transmembrane domain 3"  
 FT Domain 126..151 /note- "Intracellular domain 2"  
 FT Domain 152..171 /note- "Transmembrane domain 4"  
 FT Domain 172..193 /note- "Extracellular domain 3"  
 FT Domain 194..219 /note- "Transmembrane domain 5"  
 FT Domain 220..243 /note- "Intracellular domain 3"  
 FT Domain 244..268

FT /note= "transmembrane domain 6"  
 FT 259..280  
 FT Domain /note= "extracellular domain 4"  
 FT 281..301  
 FT Domain /note= "transmembrane domain 7"  
 FT 302..354  
 FT /note= "intracellular C-terminal domain"  
 PN MO9704094-A1.  
 XX 06-FEB-1997.  
 PD 24-JUL-1996; 96WO-FK01167.  
 PE 24-JUL-1995; 95FR-0008947.  
 XX (ADIR ) ADIR & CIE.  
 PA Jockers P. Marullo S. Stroberg AD:  
 PI WPI: 1997-132635/12.  
 DR N-PSDB: 179063-4  
 XX New nucleic acid encoding functional melatonin receptor of Xenopus -  
 PT for screening for potential (anti)agonists useful for e.g. treating  
 PT cardiovascular disease and cancer  
 PS Claim 5: Page 25-26; 62pp; French.  
 CC Sequences W25925-7 represent novel allelic Xenopus laevis melatonin  
 CC receptor MEL-1A proteins. This sequence is a new form of the melatonin  
 CC receptor designated MEL-1A, also known as Mel 1-C(alpha). The protein  
 CC differs from previously known receptors by being 65 amino acids shorter  
 CC and also having 2 different C-terminal amino acids. The protein is  
 CC encoded by 2 different alleles (179063-4) which differ in the 3'  
 CC untranslated region (both sequences encode the same protein), which is  
 CC thought to affect the half-life of the mRNA. The coding sequence was  
 CC isolated from cDNA derived from Xenopus skin RNA and amplified using the  
 CC primers T79067-76. The nucleotide sequence encodes a 7 transmembrane  
 CC receptor involved in cellular signalling. MEL-1A has been shown to  
 CC inhibit adenylyl cyclase, but both proteins can modulate intracellular  
 CC cGMP, esp. inhibiting its accumulation induced by an inhibitor of  
 CC phosphodiesterase  
 CC XX  
 SQ Sequence 354 AA:  
 Query Match 70.0% Score 1059.5; DB 18; Length 354;  
 Best Local Similarity 67.4% Pred. No. 1,1e-109;  
 Matches 190; Conservative 49; Mismatches 42; Indels 1; Gaps 1;

R88409  
 ID P88409 standard; Protein: 420 AA  
 XX  
 AC P88409;  
 XX  
 DT 15-AUG-1996 (first entry)  
 XX  
 DE High-affinity melatonin receptor.  
 XX  
 KW Melatonin receptor; G-protein-coupled receptor; glycosylation;  
 KW disulfide bond; ligand binding pocket; phosphorylation;  
 KW cytochrome-c family heme binding site; melatonin receptor-agonist;  
 KW melatonin receptor-antagonist; circadian rhythm disorder; jet lag;  
 KW day-night cycle disorder; ovulation; reproductive cycle; antibody;  
 KW animal breeding; puberty; transgenic animal; drug screening.  
 XX  
 OS Xenopus laevis.  
 FH Key Location/Qualifiers  
 FT 1..32 Domain /note= "Extracellular domain"  
 FT 5..7 Modified-site /note= "N-glycosylation site"  
 FT 16 Modified-site /note= "Protein-kinase-C phosphorylation site"  
 FT 33..57 Domain /note= "Transmembrane region-I"  
 FT 57..68 Domain /note= "Intracellular loop"  
 FT 67..72 Region /note= "Conserved melatonin receptor motif"  
 FT 69..93 Domain /note= "Transmembrane region-II"  
 FT 94..107 Domain /note= "Extracellular loop"  
 FT 105..182 Disulfide-bond /note= "Transmembrane region-III"  
 FT 108..126 Domain /note= "Protein-kinase-C phosphorylation site"  
 FT 125..131 Region /note= "Region used to construct primer"  
 FT 127..151 Domain /note= "Intracellular loop"  
 FT 132..137 Region /note= "Putative cytochrome-c family heme binding site"  
 FT 137 Modified-site /note= "Protein-kinase-C phosphorylation site"  
 FT 152..171 Domain /note= "Transmembrane region-IV"  
 FT 166 MISC-difference /note= "Residue which may form ligand binding pocket"  
 FT 172..193 Domain /note= "Extracellular loop"  
 FT 194..220 Domain /note= "Transmembrane region-V"  
 FT 204 MISC-difference /note= "Residue which may form ligand binding pocket"  
 FT 221..243 Domain /note= "Intracellular loop"  
 FT 244..268 Domain /note= "Transmembrane region-VI"  
 FT 252..259 Region /note= "Region used to construct primer"  
 FT 258 MISC-difference /note= "Residue which may form ligand binding pocket"  
 FT 259..279 Domain /note= "Extracellular loop"  
 FT 280..301 Domain /note= "Transmembrane region-VII"  
 FT 296..300 Region /note= "Conserved melatonin receptor-1b motif"  
 FT 302..420 Domain /note= "Intracellular domain"  
 FT 320 Modified-site





CC initiation or timing of puberty in humans. The receptor gene may  
CC also be expressed in a transgenic animal for use as a model system  
CC to screen agonists and antagonists.

Sequence 362 AA

Query Match:	58.88;	Score 889.5;	DB 17;	Length 362.
Best Local Similarity	-00.58;	Pred. No. 9.3e-91;		
Matches 167;	Conservative 45;	Mismatches 63;	Indels 1;	Gaps 1

```

QY 1 GNIHVSLAADIIVAAIVYPPYPLVMSINNMOMNGYLHCQSVFEMGLSVISINPTNGI 60
Db 75 qnllvslasadiivayvitypplllvallydyswa,yechekasafmgjvsgvsnlral 130
QY 61 AINNYCYIGCHSLKQCDLSESKKSLCYVLLIWLTL -AAVLENPRGTGYEPYTSCTPAQ 110
Db 135 ainyeycicshmayhnylyrwhpnlhnlclvlltvalalpntfvsyleydpriyctctiq 190
QY 120 SVSSAATIAVWVHFPLVPIIIVFCYELIWLIVQVORQKPRPKIKLPHQFQYVYMF 179
Db 195 lasklydaavvhlhllpravstcylrlwlvlgarkakpestrclqpsdlsrltmf 250
QY 180 VVWVLAICMAPLNFICGLAVADSPASWMPRPPELVFASITYAKVFNSCINAIISCYWNON 239
Db 255 vvvvllalcwaplncqlavallapmpemqrpqpeellvrtcsyllaytscnlnayvqllnqp 314
QY 240 FRKEPRRTIVSLVTAARVFVSSNDVADRKWKKPSF 275
Db 315 frreyrtrlllalmphchcldqskashaqqlspaq 350

```

```

RESULT 12
R79443
ID R79443 standard; Protein; 349 AA
XX

```

AC: P279443  
XX

DT 17-JAN-1996 (first entry)  
XX

DE Galanin receptor  
XY

KW valinin receptor; gene; antibody; analgesic; probe; detection  
 KW diagnosis; neurological disorder; endocrine disorder,  
 KW psychiatric disorder; gene expression; ds.

*Homo sapiens.*

PN FR2716,205-A1.  
XY

PH: H-ALG-1995.

PF : 7-FHH-1994: 94FR-0001808.

PR 17-PH-1994; 94FR-0001808

IPA (KHON) KHON: POLLEN: ROFFR SA.  
XX

PI Amiranolt B, Habert-ortoli E, Loquet I, vx

DR WP1; 1995-285172/38.

DR N-PSDH; Q97304

PT New galanin receptor gene - useful for diagnosing neurological, cardiovascular, endocrine or psychiatric disorders.

Claim 8; Page 15-18; 27pp; French.

Galactinergic receptors are useful as biological and pharmacological research tools and for production of antibodies. Analogs of such receptors are useful as analgesics. Probes directed against the gene are useful for detecting expression of galactinergic receptors for detecting genetic abnormalities, for diagnosing neurological,

CC cardiovascular, endocrine or psychiatric disorders and for detecting  
CC and isolating nucleic acid sequences coding for galaninergic  
CC polypeptides.  
XY

SQ Sequence 349 AA

Query Match	18.8%	Score	285	DP	16	Length	349
Best Local Similarity	26.38%	Pred. No.	1.5e-23				
Matches	76	Conservative	62	Mismatches	129	Indels	22
						Gaps	6

[illegible]

```

RESULT 13
R95070
ID R95070 standard; Protein; 349 AA.
VY

```

AC R95070;

DT 27-OCT-1996 (first entry)  
XX

Human galanin receptor

KW Galanin receptor; stomach ulcer; antiulcer; diabetes; antidiabetic  
KW dementia; neuropeptide; sedative; Alzheimer's disease  
XX

OS Homo sapiens.

PN EP711830-A2.  
XX

PD 15-MAY-1996

PF	11-OCT-1995	95EP-0115996
XX		

PR	01-MAY-1993;	95JP-0134412
PR	13-OCT-1994;	94TP-0247599

XX

FF (NAME) JANEDA CHEM IND LTD  
XX

PI Fujii K, Fukusumi S, Hinuma  
PI Ohtaki T, Onda H.

XX

WP1: T2995-252095/24.  
N-PSDB: T29436

XX

agonists or antagonists, which can be used to treat, e.g. ulcers, diabetes or dementia

PS Claim 1; Page 48-50; 71pp; English.  
xx

CC This sequence encoding a human galanin receptor protein may be  
CC expressed recombinantly in e.g. CHO cells. This protein is

CC particularly used to identify agonists or antagonists which can be  
CC used to treat e.g. ulcers, diabetes or dementia, etc. The protein  
CC can also be used for the detection of galanin in the production of  
CC antibodies and transgenic animals

XX Sequence 349 AA

Query Match 18.8% Score 285 DB 17 Length 346  
Best Local Similarity 26.3% Pred. No. 1-5e-23  
Matches 75 Conservative 52 Mismatches 129 Indels 22 Gaps 6

QY 2 NIPVSLVADLVVAIVYPLVMSIFNNMNLGYHGVSGFLMGLSVISGHNIGIA 61  
DB 71 NIIINSLADLAIYIIICIFGATYALPTWIIQATICKIHYITVSMIVSITILAAIS 130  
QY 62 INPYVYCHSKDKYSSKNSGYVILIMLTAAVIPNIPTQIQYPPYVSPVAVSV 171  
DB 131 VHYVAIYHSTRESLVSSTALIVGCIWASLMSAPYHQIIPRISNQIQWQ 190  
QY 122 -----SSAVTAVVVFHVLPMIVIPYLPIMLVQVQPVPPKPKIKHPDENP 175  
DB 131 WDPDHHKAYVCTCFYIIPIIIICCTGKVVVILIMLKKLYGMSKSSQIKKLA 246  
QY 176 VIMFVFLFALICWAPLNFIS-----AVASIPASMPPIPEMLFVAYVAVNSGNA 230  
DB 247 GIVVWVWVIGVIGVPHIILWAGGQIFIFASGIFIT-----TQHIYVFSQV 300  
QY 271 IISTWNNFREFEPIVSLVAVFVDSNVAQSVKKSELMN 279  
DB 301 IIVATISENTKAYKGVCHIRKSDSLKQV-KSTIDFPTSGVTH 349

#### RESULT 14

Y45129 standard: Protein; 346 AA.

Y45129:

21-DEC-1999 (first entry)

Rat galanin receptor 1.

Physiologically active peptide; receptor binding; galanin receptor;

GALR1; GALR2; GALR3; Oryzotrypsin 11a and; Preprogalanin; galanin;

drug development; memory function; appetite; improve; womb; kidney;

function regulator; prostate; testis; skeletal muscle.

Rattus sp.

W09948920-A1.

24-MAR-1999: 99WC-JP01482.

25-MAR-1999: 99JP-0074-49

21-SEP-1998: 98JP-0266972.

(TAKE ) TAKEDA CHEM IND LTD.

Ohkaki T, Matsui H, Ishibashi Y, Ogi K, Kitada C;

WPI: 1999-572170/48.

N-PSDB: 225518.

Peptides binding to galanin receptor proteins, used to, e.g. improve

kidney functioning.

Claim 1: Page 119-121, 153pp; Japanese.

The present invention describes peptides (1) binding to galanin receptor

proteins (1) contain the sequence AAHHSPDQ or one substantially

CC identical to it, and their precursors, salts, amides and esters, which  
CC kind especially to rat galanin receptor proteins. Products from the  
CC present invention are used in assays of galanin/galanin receptor binding  
CC and the development of drugs acting on galanin binding, such as memory  
CC function improvers, appetite improvers, and function regulators for the  
CC womb, kidney, prostate, testis or skeletal muscle. Y45129 to Y45154 and  
CC 22519 to 22552 represent sequences used in the exemplification of  
CC the present invention.

XX Sequence 346 AA:

Query Match 18.6% Score 281 DB 20 Length 346  
Best Local Similarity 28.0% Pred. No. 4.1e-23  
Matches 73 Conservative 57 Mismatches 101 Indels 40 Gaps 7

QY 2 NIPVSLVADLVVAIVYPLVMSIFNNMNLGYHGVSGFLMGLSVISGHNIGIA 61  
DB 70 NIIINSLADLAIYIIICIFGATYALPTWIIQATICKIHYITVSMIVSITILAAIS 129  
QY 62 INPYVYCHSKDKYSSKNSGYVILIMLTAAVIPNIPTQIQYPPYVSPVAVSV 117  
DB 130 VHYVAIYHSTRESLVSSTALIVGCIWASLMSAPYHQIIPRISNQIQWQ 184  
QY 118 A-----QVSSAVTAVVVFHVLPMIVIPYLPIMLVQVQPVPPKPKIKHPDENP 171  
DB 139 WDPDHHKAYVCTCFYIIPIIIICCTGKVVVILIMLKKLYGMSKSSQIKKLA 240  
QY 172 FNNVIMFVFLFALICWAPLNFIS-----AVASIPASMPPIPEMLFVAYVAVNSGNA 235  
DB 241 GIVVWVWVIGVIGVPHIILWAGGQIFIFASGIFIT-----TQHIYVFSQV 294  
QY 227 CLNATISGVWNNCFEKPRI 247  
DB 295 STWPIYATISENTKAYKGV 315

#### RESULT 15

R95069 standard: Protein; 348 AA.

R95069:

27-OCT-1996 (first entry)

Mouse pancreas beta-cell line MIN6 galanin receptor.

galanin receptor; stomach ulcer; antidiabetic; diabetes; antidiabetic;

dementia; neuroptide; sedative; Alzheimer's disease.

Mus musculus.

EP711830-A2.

15-MAY-1996.

21-OCT-1995: 95EP-0718996.

31-MAY-1995: 95JP-0134412.

13-OCT-1994: 94JP-0247599.

28-DEC-1994: 94JP-0326610.

(TAKE ) TAKEDA CHEM IND LTD.

Fujii K, Fukusumi S, Hinuma S, Hosoya M, Ohai K;

Ohkaki T, Onda H;

WPI: 1996-230065/24.

N-PSDB: T29435.

Isolated galanin receptor proteins, used partic. to identify

agonists or antagonists, which can be used to treat e.g. ulcers

diabetes or dementia

XX Claim 1: Page 46: 71pp: English.

CC This sequence encoding a mouse galanin receptor protein was obtained  
 CC from the mouse pancreatic beta-cell line, MIN6 (FERM BP-4954), and  
 CC may be expressed recombinantly in e.g. CHO cells. This protein is  
 CC particularly used to identify agonists or antagonists which can be  
 CC used to treat e.g. ulcers, diabetes or dementia, etc. The protein  
 CC can also be used for the detection of galanin, in the production of  
 CC antibodies, and transgenic animals.

XX Sequence 348 AA:

Query Match 18.4% Score 279; DB 17; Length 348;  
 Best Local Similarity 26.8% Prod No 6,9e-23;  
 Matches 70; Conservative 58; Mismatches 103; Indels 30; Gaps 6;

QY 2 NIFVSLAVADLVVAIYPPVPLVLSIFNNGNLCYLCQVSGFLMGLSVIGSIFNITGIA 61  
 DB 71 nifslsladlvalyppvplvlsifnngnlyclhqvsgflmglsvigisifnitgia 61  
 QY 62 INRGYICHSLSKCKLSSKSLCYVLLIMLTAAVLPLRGTLQYEPRIYSGTFAQSV 121  
 DB 131 inrgyicshslskcklsskslcyvllimltaaavlplrgtlqyepriysgtfaosv 121  
 QY 122 -----SSAYTIAVVFHFPLVPMIIVFCYLRIMILVQVRQKDPDRKPKLPHD 171  
 DB 186 cweqmpnrlhprayveclivqylpllllclcyakv---lnhlkklk-nmskksask 241  
 QY 172 FRNFVIMKVVVLAICAPLNFGL----AVASPRASKVPRIPENLFFVASYMAYFNS 226  
 DB 242 kktatfvlyvvvqlqslwphvwhlwaefadplpdsffrl-----tanclaysns 295  
 QY 227 CINAIISGMNQNPFKEYPRI 247  
 DB 296 scnpilgafisontfkaykqv 316

Search completed: February 19, 2001, 20:18:11  
 Job time: 12781 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: February 18, 2001, 14.31.06 : Search time 54.18 seconds  
(without alignments)  
95.453 Million cell updates/sec

Title: US-09-226-046-6  
Sequence: 1 GNFVSVSLAVADLVAIPY..... VKKPSPLMNNVVKVDSV 288  
1514

Scoring table:  
Gapop 10.0, Gapext 0.5

Searched: 174772 seqs, 17957048 residues  
Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database: Issued Patents AA:  
1: /cgn2\_6/prodata/2/1a3/5A.COMB.pep.\*  
2: /cgn2\_6/prodata/2/1a3/5R.COMB.pep.\*  
3: /cgn2\_6/prodata/2/1a3/5.COMB.pep.\*  
4: /cgn2\_6/prodata/2/1a3/PTTUS.COMB.pep.\*  
5: /cgn2\_6/prodata/2/1a3/backfill1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1514	100.0	288	2 US-08-466-103A-6	Sequence 6, Appl
2	1443.5	95.3	350	2 US-08-466-103A-12	Sequence 12, Appl
3	1443.5	95.3	353	2 US-08-896-365-6	Sequence 6, Appl
4	1308.5	86.4	353	2 US-09-280-420-2	Sequence 2, Appl
5	1292.5	85.4	353	2 US-08-466-103A-14	Sequence 14, Appl
6	1241.5	82.0	366	2 US-08-466-103A-4	Sequence 7, Appl
7	1241.5	82.0	366	2 US-08-896-365-7	Sequence 8, Appl
8	1109.5	73.3	257	2 US-08-896-365-8	Sequence 2, Appl
9	1059.5	70.0	420	2 US-08-466-103A-16	Sequence 16, Appl
10	689.5	58.8	362	2 US-08-466-103A-16	Sequence 9, Appl
11	689.5	58.8	362	2 US-08-896-365-9	Sequence 16, Appl
12	285	18.8	351	3 US-08-513-974B-344	Sequence 34, App
13	281	18.6	349	3 US-08-513-974B-343	Sequence 34, App
14	279	18.4	348	3 US-08-513-974B-46	Sequence 46, Appl
15	279	18.4	348	3 US-08-513-974B-342	Sequence 34, App
16	261	17.2	391	3 US-08-676-351-4	Sequence 4, Appl
17	260	17.2	391	3 US-08-454-544-3	Sequence 3, Appl
18	260	17.2	391	3 US-08-454-544-3	Sequence 3, Appl
19	260	17.2	398	1 US-08-149-093A-5	Sequence 5, Appl
20	260	17.2	398	1 US-08-911-245-5	Sequence 5, Appl
21	260	17.2	398	3 US-08-889-108-2	Sequence 2, Appl
22	260	17.2	398	3 US-08-889-108-2	Sequence 2, Appl
23	259	17.0	398	4 PCT-US84-10358-2	Sequence 26, Appl
24	259	17.0	398	4 PCT-US84-10358-2	Sequence 32, App
25	257.5	17.0	400	3 US-08-513-974B-323	Sequence 8, Appl
26	257.5	17.0	400	3 US-08-889-108-8	Sequence 8, Appl
27	251.5	16.6	303	4 PCT-US94-10358-8	Sequence 9, Appl
28	251.5	16.6	303	4 US-08-196-989B-9	Sequence 9, Appl
				2 US-08-750-936-9	Sequence 9, Appl

29	244.5	16.1	388	1 US-08-087-772A-2	Sequence 2, Appl
30	244.5	16.1	400	1 US-08-351-473B-5	Sequence 5, Appl
31	241	15.9	398	3 US-09-170-331-5	Sequence 1, Appl
32	239.5	15.8	400	1 US-07-783-602C-1	Sequence 1, Appl
33	238.5	15.8	405	1 US-08-351-473B-2	Sequence 2, Appl
34	238	15.7	483	1 US-08-194-338-7	Sequence 7, Appl
35	237.5	15.7	400	1 US-07-916-901-6	Sequence 6, Appl
36	237.5	15.7	400	1 US-08-351-473B-4	Sequence 4, Appl
37	234	15.5	372	2 US-08-626-685A-8	Sequence 2, Appl
38	233.5	15.4	384	1 US-09-045-186-2	Sequence 4, Appl
39	233.5	15.4	384	2 US-08-232-144-4	Sequence 15, Appl
40	233.5	15.4	384	2 US-08-555-269A-15	Sequence 3, Appl
41	233.5	15.4	384	2 PCT-US93-05039-3	Sequence 3, Appl
42	233	15.4	513	4 US-08-406-883A-21	Sequence 21, Appl
43	233	15.4	513	3 US-09-206-899-21	Sequence 21, Appl
44	232	15.3	515	1 US-08-444-734A-7	Sequence 7, Appl
45	232	15.3	515	2 US-08-406-855A-22	Sequence 22, Appl

## ALIGNMENTS

## RESULT 1

US-08-466-103A-6  
Sequence 6, Application US/08466103A

Patent No. 5856124

GENERAL INFORMATION:  
APPLICANT: Reperit, Steven M.

APPLICANT: Edisawa, Takashi  
TITLE OF INVENTION: HIGH-AFFINITY MELANOTIN  
RECEPTORS AND USES THEREOF

NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA

COUNTRY: US  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette

COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95

SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,103A

FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435

Prior APPLICATION DATA:  
APPLICATION NUMBER: 08/319,887  
FILING DATE: 07-OCT-1994

Prior APPLICATION DATA: 08/261,857  
APPLICATION NUMBER: 08/319,887  
FILING DATE: 17-JUN-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 00786/250002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal

US-08-466-103A-6

Query Match 100.0% Score 1514, DB 2, Length 288:  
Best Local Similarity 100.0% Pred. No. 4,1e+126:

Matches: 288; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0

QY 1 GNFVSLAVADLVVAIYIPYPLVMSIFNNGNMLCYLHGVSGFLMGSLVISIFNITGI 60  
 DB 1 GNFVSLAVADLVVAIYIPYPLVMSIFNNGNMLCYLHGVSGFLMGSLVISIFNITGI 60

QY 61 AINRYCYICHSLCKDKLYSKNSLCYVLLIWLITAAVLPNLRGTLQYEPPIYCTFAQS 120  
 DB 61 AINRYCYICHSLCKDKLYSKNSLCYVLLIWLITAAVLPNLRGTLQYEPPIYCTFAQS 120

QY 121 SVSASATIAVAVFHFLVPMILVIFCYLPIWILVQVOPKPKPKPKPKPKPKPKPKPKPK 180  
 DB 121 SVSASATIAVAVFHFLVPMILVIFCYLPIWILVQVOPKPKPKPKPKPKPKPKPKPKPK 180

QY 181 VVFLFAICWAPLNFITGLAVASDPASWVPRIPEMLFVASYMAFNSCLNAILISGYWNONF 240  
 DB 181 VVFLFAICWAPLNFITGLAVASDPASWVPRIPEMLFVASYMAFNSCLNAILISGYWNONF 240

QY 241 KKRYPRILVSLTARVFFVDSNDVADRYKKRPSPLMTNNNNVKKVDSV 288  
 DB 241 KKRYPRILVSLTARVFFVDSNDVADRYKKRPSPLMTNNNNVKKVDSV 288

## RESULT 2

US-08-466-103A-12  
 Sequence 12, Application US/04466-103A

GENERAL INFORMATION:  
 PATENT NO. 5856124  
 APPLICANT: Reppert, Steven M.  
 APPLICANT: Edisawa, Takashi  
 TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
 TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: US  
 ZIP: 02110-2804

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows95  
 SOFTWARE: FASTA for Windows Version 2.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/04466-103A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/319,487  
 FILING DATE: 07-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/221,457  
 FILING DATE: 17-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Janis K.  
 REGISTRATION NUMBER: 34,819  
 REFERENCE: DOCPT NUMBER: 00866-0250002

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/642-5070  
 TELEFAX: 617/642-8906  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 350 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: integral  
 US-08-466-103A-12

Query Match: 95.3%; Score: 1443.5; DH: 2; Length: 350;

Fast Local Similarity: 96.9%; Prod. No. 99-120;  
 Matches: 280; Conservative: 1; Mismatches: 7; Indels: 1; Gaps: 1;

QY 1 GNFVSLAVADLVVAIYIPYPLVMSIFNNGNMLCYLHGVSGFLMGSLVISIFNITGI 60  
 DB 62 GNFVSLAVADLVVAIYIPYPLVMSIFNNGNMLCYLHGVSGFLMGSLVISIFNITGI 121

QY 61 AINRYCYICHSLCKDKLYSKNSLCYVLLIWLITAAVLPNLRGTLQYEPPIYCTFAQS 119  
 DB 122 AINRYCYICHSLCKDKLYSKNSLCYVLLIWLITAAVLPNLRGTLQYEPPIYCTFAQS 181

QY 120 SVSASATIAVAVFHFLVPMILVIFCYLPIWILVQVOPKPKPKPKPKPKPKPKPKPKPK 179  
 DB 182 SVSASATIAVAVFHFLVPMILVIFCYLPIWILVQVOPKPKPKPKPKPKPKPKPKPKPK 241

QY 180 VVFLFAICWAPLNFITGLAVASDPASWVPRIPEMLFVASYMAFNSCLNAILISGYWNONF 239  
 DB 242 VVFLFAICWAPLNFITGLAVASDPASWVPRIPEMLFVASYMAFNSCLNAILISGYWNONF 301

QY 240 KKRYPRILVSLTARVFFVDSNDVADRYKKRPSPLMTNNNNVKKVDSV 288  
 DB 302 KKRYPRILVSLTARVFFVDSNDVADRYKKRPSPLMTNNNNVKKVDSV 350

## RESULT 3

US-08-695-365-6

Sequence 6, Application US/08695365  
 Patent No. 5934264

GENERAL INFORMATION:  
 APPLICANT: Rothschild, Max F.  
 APPLICANT: Tugale, Christopher K.  
 APPLICANT: Messer, Lori A.  
 APPLICANT: Tun-Ping, Yu  
 TITLE OF INVENTION: GENES AND GENOTYPIC MARKERS FOR IMPROVED  
 TITLE OF INVENTION: REPRODUCTIVE TRAITS IN ANIMALS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Zarley, McKee, Thomete, Voorhees & Sease  
 STREET: 801 Grand Avenue, Suite 3200  
 CITY: Des Moines  
 STATE: Iowa  
 COUNTRY: USA  
 ZIP: 50309

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/695,365  
 FILING DATE: 18-JUL-1997  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/60/023,180  
 FILING DATE: 19-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nebel, Heidi S.  
 REGISTRATION NUMBER: 37,719  
 REFERENCE: DOCPT NUMBER: ISUPF 021591

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 515-288-3667  
 TELEFAX: 515-288-1338  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 353 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens

CELL TYPE: Melanocyte  
CELL LINE: human melatonin receptor 1a  
POSITION IN GENOME:  
MAP POSITION: 14  
US-08-896-365-6

Query Match 95.38 Score 1443.5 DB 2 Length 353  
Best Local Similarity 96.28, Fred. No. 8.1e-120  
Matches 280; Conservative 1; Mismatches 7; Indels 1; Gaps 1

QY 1 GNIFVSLAVADLVVAIIPYPLVLMSTFNNNGMNLGYLHCQVSGFLMGLSVISFNTGI 60  
DB 65 GNIFVSLAVADLVVAIIPYPLVLMSTFNNNGMNLGYLHCQVSGFLMGLSVISFNTGI 124  
QY 61 AINPCYICHSKCKKIKYSSKNSLCYVLLIMLT-AAVLEPMLPGTLQYEPPIYSCFPAQ 119  
DB 125 AINPCYICHSKCKKIKYSSKNSLCYVLLIMLTAAVLEPMLPGTLQYDPRIYSCFPAQ 184  
QY 120 SVSSAYTIAVVVFHEFLVPMIIVFCYLRILWLVLYQVPRPVKPKPKPKPHDFRNFVTMF 179  
DB 185 SVSSAYTIAVVVFHEFLVPMIIVFCYLRILWLVLYQVPRPVKPKPKPKPHDFRNFVTMF 244  
QY 180 VVFLVFAICMAPLNLIGLAVASDPASWPRIPEMLEFVASYMAVFNSCLNAIISGYWNON 239  
DB 245 VVFLVFAICMAPLNLIGLAVASDPASWPRIPEMLEFVASYMAVFNSCLNAIISGYWNON 304  
QY 240 FRKEXRIIVSLVTARVFVDSNDVADRVKPKPSPLMTNNNVKVDV 288  
DB 305 FRKEXRIIVSLVTARVFVDSNDVADRVKPKPSPLMTNNNVKVDV 353

RESULT 4  
US-09-280-420-2  
Sequence 2 Application US/09280420  
Patent No. 6037131

GENERAL INFORMATION:  
APPLICANT: Reppert, Steven M.  
TITLE OF INVENTION: MELATONIN 1A RECEPTOR GENE  
TITLE OF INVENTION: REGULATORY PROTEINS AND USES THEREOF  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/280.420  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/895,701  
FILING DATE:  
APPLICATION NUMBER: 60/022,155  
FILING DATE: 18-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00786/340002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-507  
TELEFAX: 617/542-890  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 353 amino acids

TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-09-280-420-2

Query Match 86.48; Score 1308.5; DB 3 Length 353  
Best Local Similarity 84.48; Fred. No. 6.1e-108  
Matches 244; Conservative 25; Mismatches 19; Indels 1; Gaps 1

QY 1 GNIFVSLAVADLVVAIIPYPLVLMSTFNNNGMNLGYLHCQVSGFLMGLSVISFNTGI 60  
DB 65 GNIFVSLAVADLVVAIIPYPLVLMSTFNNNGMNLGYLHCQVSGFLMGLSVISFNTGI 124  
QY 61 AINPCYICHSKCKKIKYSSKNSLCYVLLIMLT-AAVLEPMLPGTLQYEPPIYSCFPAQ 119  
DB 125 AINPCYICHSKCKKIKYSSKNSLCYVLLIMLTAAVLEPMLPGTLQYDPRIYSCFPAQ 184  
QY 120 SVSSAYTIAVVVFHEFLVPMIIVFCYLRILWLVLYQVPRPVKPKPKPKPHDFRNFVTMF 179  
DB 185 SVSSAYTIAVVVFHEFLVPMIIVFCYLRILWLVLYQVPRPVKPKPKPKPHDFRNFVTMF 244  
QY 180 VVFLVFAICMAPLNLIGLAVASDPASWPRIPEMLEFVASYMAVFNSCLNAIISGYWNON 239  
DB 245 VVFLVFAICMAPLNLIGLAVASDPASWPRIPEMLEFVASYMAVFNSCLNAIISGYWNON 304  
QY 240 FRKEXRIIVSLVTARVFVDSNDVADRVKPKPSPLMTNNNVKVDV 288  
DB 305 FRKEXRIIVSLVTARVFVDSNDVADRVKPKPSPLMTNNNVKVDV 353

RESULT 5  
US-08-466-103A-14  
Sequence 14 Application US/08466103A  
Patent No. 5856124

GENERAL INFORMATION:  
APPLICANT: Reppert, Steven M.  
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466.103A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/315,887  
FILING DATE: 07-OCT-1994  
APPLICATION NUMBER: 08/261,857  
FILING DATE: 17-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/DOCKET NUMBER: 00786/250002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5076  
TELEFAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:

LENGTH: 452 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-466-103A-14

Query Match 85.4% Score 1292.5 DB 2 Length 353  
 Best Local Similarity 83.7% Pctd No. 166-106  
 Matches 242 Conservative 24 Mismatches 22 Indels 1 Gaps 1

UY 1 GNIFVSLAVADLVVAIVYPPYLVLSIFNNGNGLYLCQVSGFMGLSVGISTNITGI 60  
 DB 65 GNIFVSLAVADLVVAIVYPPYLVLSIFNNGNGLYLCQVSAFLMGLSVGISTNITGI 124  
 UY 61 AINRVCYICHSKCKLYSKNSKSLCYVLLIMLT-AAVLPNLRPTLYEPPIYSCFPAQ 119  
 DB 125 AINRVCYICHSKCKLYSKNSKSLCYVLLIMLTAAVLPNLRPTLYEPPIYSCFPAQ 184  
 UY 120 SVSAYTIAVVFHPLVPMIVIPCYLRIMLVLOVRORVPRPKPKLPHDFRNFVTMF 179  
 DB 185 SVSAYTIAVVFHPLVPMIVIPCYLRIMLVLOVRORVPRPKPKLPHDFRNFVTMF 244  
 UY 180 VVFLFAICWALNLTGLAVASDPASMPRIPEMLFVASVYMAVFNLSCLNATISGMWON 239  
 DB 245 VVFLFAICWALNLTGLAVASDPASMPRIPEMLFVASVYMAVFNLSCLNATISGMWON 304  
 UY 240 FPEYPRIVSLTAVVFVDSNDVADRVKWPSPPLMTNNVAVVDSV 288  
 DB 405 FPEYPRIVSLTAVVFVDSNDVADRVKWPSPPLMTNNVAVVDSV 353

RESULT 6  
 US-08-466-103A-4  
 Sequence 4, Application US/08466103A  
 Patent No. 5856124

## GENERAL INFORMATION:

APPLICANT: Reppert, Steven M.  
 APPLICANT: Edisawa, Takashi  
 TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA

COUNTRY: US  
 ZIP: 02110-2804

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466.103A  
 FILING DATE: 06-JUN-1995

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/419,897  
 FILING DATE: 07-OCT-1994

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/419,897

ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Janis K.

REGISTRATION NUMBER: 34,819  
 REFERENCE/DOCKET NUMBER: 00786/250002

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 366 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-466-103A-4

Query Match 92.0% Score 1241.5 DB 2 Length 366  
 Best Local Similarity 89.6% Pctd No. 60-102  
 Matches 233 Conservative 25 Mismatches 30 Indels 1 Gaps 1

UY 1 GNIFVSLAVADLVVAIVYPPYLVLSIFNNGNGLYLCQVSGFMGLSVGISTNITGI 60  
 DB 78 GNIFVSLAVADLVVAIVYPPYLVLSIFNNGNGLYLCQVSAFLMGLSVGISTNITGI 137  
 UY 61 AINRVCYICHSKCKLYSKNSKSLCYVLLIMLT-AAVLPNLRPTLYEPPIYSCFPAQ 119  
 DB 138 AINRVCYICHSKCKLYSKNSKSLCYVLLIMLTAAVLPNLRPTLYEPPIYSCFPAQ 197  
 UY 120 SVSAYTIAVVFHPLVPMIVIPCYLRIMLVLOVRORVPRPKPKLPHDFRNFVTMF 179  
 DB 198 SVSAYTIAVVFHPLVPMIVIPCYLRIMLVLOVRORVPRPKPKLPHDFRNFVTMF 257  
 UY 180 VVFLFAICWALNLTGLAVASDPASMPRIPEMLFVASVYMAVFNLSCLNATISGMWON 239  
 DB 258 VVFLFAICWALNLTGLAVASDPASMPRIPEMLFVASVYMAVFNLSCLNATISGMWON 317  
 UY 240 FPEYPRIVSLTAVVFVDSNDVADRVKWPSPPLMTNNVAVVDSV 288  
 DB 318 FPEYPRIVSLTAVVFVDSNDVADRVKWPSPPLMTNNVAVVDSV 366

RESULT 7  
 US-08-896-365-7  
 Sequence 7, Application US/08896365  
 Patent No. 5939264

## GENERAL INFORMATION:

APPLICANT: Rothschild, Max F.  
 APPLICANT: Tugale, Christopher K.  
 APPLICANT: Messel, Lori A.  
 TITLE OF INVENTION: GENES AND GENETIC MARKERS FOR IMPROVED  
 TITLE OF INVENTION: REPRODUCTIVE TRAITS IN ANIMALS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Bailey, McKee, Thorne, Vothrees & Sease  
 STREET: 801 Grand Avenue, Suite 3200  
 CITY: Des Moines  
 STATE: Iowa

COUNTRY: USA  
 ZIP: 50309

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/896.365  
 FILING DATE: 18-JUL-1997

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 68/032,187  
 FILING DATE: 19-JUL-1996

ATTORNEY/AGENT INFORMATION:  
 NAME: Nebel, Heidi S.

REGISTRATION NUMBER: 37,719  
 REFERENCE/DOCKET NUMBER: ISHF 021591

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 515-288-3667

TELEFAX: 515-288-1338

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 366 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Ovis ammon aries  
 CELL TYPE: Melanocyte  
 US-08-896-365-7

Query Match 82.0%; Score 1241.5; DB 2: Length 366;  
 Best Local Similarity 80.6%; Pred. No. 5e-102;  
 Matches 233; Conservative 25; Mismatches 30; Indels 1; Gaps 1;

1 GNIFVSLAVADLVVAIPYPLVLMIFNNGWNLGYHCVSGFLMGSLVGSIFNTGI 60  
 78 GNIFVSLAVADLVVAIPYPLVLMIFNNGWNLGYHCVSGFLMGSLVGSIFNTGI 137  
 61 ANFCYICHSIKCKDKVSKSKSLCYLLMLT-AAVLPMLPBGTLQYEPRIYCTFAQ 119  
 138 ANFCYICHSIKCKDKVSKSKSLCYLLMLT-AAVLPMLPBGTLQYEPRIYCTFAQ 197  
 120 SYSSATTAIVVVEHELVPMIIVFCYLRIMVLVQVPPVPRDKPKPKPHDFNFVTME 179  
 198 SYSSATTAIVVVEHELVPMIIVFCYLRIMVLVQVPPVPRDKPKPKPHDFNFVTME 257  
 180 VYVVLFAICMAFLNFGCLVAVSGPASPMPPIPEMLFVASYMAVFNCLNAIISGYWNON 239  
 258 VYVVLFAICMAFLNFGCLVAVSGPASPMPPIPEMLFVASYMAVFNCLNAIISGYWNON 317  
 240 FKEEYFPIIVSTVTAPEFVDSNVDAPVKKFSEFLMTNNNVAVDEV 288  
 318 FKEEYFPIIVSTVTAPEFVDSNVDAPVKKFSEFLMTNNNVAVDEV 366

RESULT 8  
 US-08-896-365-8  
 Sequence 8, Application US/08896365  
 Patent No. 5939264  
 GENERAL INFORMATION:  
 APPLICANT: Rothschild, Max F.  
 APPLICANT: Tugler, Christopher K.  
 APPLICANT: Messer, Lori A.  
 APPLICANT: Tun-Ping, Yu  
 TITLE OF INVENTION: GENES AND GENETIC MARKERS FOR IMPROVED  
 TITLE OF INVENTION: REPRODUCTIVE TRAITS IN ANIMALS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease  
 STREET: 801 Grand Avenue, Suite 3200  
 CITY: Des Moines  
 STATE: Iowa  
 COUNTRY: USA  
 ZIP: 50309  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/896,365  
 FILING DATE: 18-JUL-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/022,180  
 FILING DATE: 19-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nebel, Heidi S.  
 REGISTRATION NUMBER: 37,719

REFERENCE/DOCKET NUMBER: ISURF 021591  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 515-288-3667  
 TELEFAX: 515-288-1338  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 257 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Bos taurus  
 CELL TYPE: Melanocyte  
 US-08-896-365-8

Query Match 73.3%; Score 1109.5; DB 2: Length 257;  
 Best Local Similarity 81.3%; Pred. No. 1.4e-90;  
 Matches 209; Conservative 19; Mismatches 28; Indels 1; Gaps 1;

20 YPLVMSIFNNGWNLGYHCVSGFLMGSLVGSIFNTGIAINPYCICHSIKCKDKLS 79  
 1 YPLVMSIFNNGWNLGYHCVSGFLMGSLVGSIFNTGIAINPYCICHSIKCKDKLS 138  
 80 SNNSCYLLMLT-AAVLPMLPBGTLQYEPRIYCTFAQSYSSATTAIVVVEHELVPM 138  
 61 SNNSCYLLMLT-AAVLPMLPBGTLQYEPRIYCTFAQSYSSATTAIVVVEHELVPM 120  
 139 IVICCYLRIMVLVQVPPVPRDKPKPKPHDFNFVTMEVVLFAICMAFLNFGCLV 198  
 121 IVICCYLRIMVLVQVPPVPRDKPKPKPHDFNFVTMEVVLFAICMAFLNFGCLV 180  
 199 VASDPASVPIPEMLFVASYMAVFNCLNAIISGYWNONFKEEYFPIIVSTVTAPE 258  
 181 VASDPASVPIPEMLFVASYMAVFNCLNAIISGYWNONFKEEYFPIIVSTVTAPE 240  
 259 VDSNDVADRVKKRPS 275  
 241 VDSNDVADRVKKRPS 257

RESULT 9  
 US-08-466-103A-2  
 Sequence 2, Application US/08466103A  
 Patent No. 5856124  
 GENERAL INFORMATION:  
 APPLICANT: Reppert, Steven M.  
 APPLICANT: Ebisawa, Takashi  
 TITLE OF INVENTION: HIGH-AFFINITY MELANOTININ  
 TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: US  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: Windows95  
 SOFTWARE: FASTED for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,103A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/319,887  
 FILING DATE: 07-OCT-1994

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/261,857  
 FILING DATE: 17-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Janis K.  
 REGISTRATION NUMBER: 44,819  
 REFERENCE/DOCKET NUMBER: 00786/250002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 420 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-466-103A-2

Query Match 70.0% Score 1059.5; DB 2; Length 420;  
 Best Local Similarity 67.4%; Pred. No. 6e-86;  
 Mismatches 42; Indels 1; Gaps 1;

1 GNIFVSLAVADLVAVIPYPLVLSIFNNNGNLGYLHCQVSGFLMGISVIGSIFNIGI 60  
 67 GNLFVSLADLVAVIPYPLVLAIFQNGTLDGHLGSLGSLVSGVFNITAI 126  
 61 AINRYCYICHSKCDKSLKSKSLCYLLIWLTTAAVLPNLRGTDYEPRIYSCITFAQ 119  
 127 AINRYCYICHSKSLKSKSLKSKSLCYLLIWLTTAAVLPNLRGTDYEPRIYSCITFAQ 186  
 120 SVSSATTAAVVFHFLVPMIIVFCYLPRIWLVQVQVKKPKPKPKHPRFVTFMF 179  
 147 TVSSVTTTAAVVFHFLVPMIIVFCYLPRIWLVQVQVKKPKPKPKHPRFVTFMF 246  
 140 VVFLFAICMAPLNFICGLAVASDPASMPRIPEMLFVASYMAYFNSCLNAIISGYWNN 239  
 247 VVFLFAICMAPLNFICGLAVAINPFAVAPKIDEMLFVLSYMAFYNSCLNAIISGYWNN 306  
 240 FKEEYPRILVLTAVVFVDSSTAVAPVKKPSP 281  
 407 FKEEYPRILVLTAVVFVDSSTAVAPVKKPSP 348

RESULT 10  
 US-08-466-103A-16  
 Sequence 16, Application US/08466103A

Patent No. 5856124  
 GENERAL INFORMATION:  
 APPLICANT: Report, Steven M.  
 APPLICANT: Ebisawa, Takashi  
 TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
 TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: US  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows95  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,103A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/319,887

FILING DATE: 07-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/261,857  
 FILING DATE: 17-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Janis K.  
 REGISTRATION NUMBER: 44,819  
 REFERENCE/DOCKET NUMBER: 00786/250002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8906  
 INFORMATION FOR SEQ ID NO: 16:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 362 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-466-103A-16

Query Match 58.8% Score 889.5; DB 2; Length 362;  
 Best Local Similarity 60.9%; Pred. No. 4.7e-71;  
 Matches 167; Conservative 45; Mismatches 63; Indels 1; Gaps 1;

1 GNIFVSLAVADLVAVIPYPLVLSIFNNNGNLGYLHCQVSGFLMGISVIGSIFNIGI 60  
 75 GNLFVSLADLVAVIPYPLVLAIFQNGTLDGHLGSLGSLVSGVFNITAI 134  
 61 AINRYCYICHSKCDKSLKSKSLCYLLIWLTTAAVLPNLRGTDYEPRIYSCITFAQ 119  
 135 AINRYCYICHSKSLKSKSLKSKSLCYLLIWLTTAAVLPNLRGTDYEPRIYSCITFAQ 194  
 120 SVSSATTAAVVFHFLVPMIIVFCYLPRIWLVQVQVKKPKPKPKHPRFVTFMF 179  
 195 TASTQYTAAVVFHFLVPMIIVFCYLPRIWLVQVQVKKPKPKPKHPRFVTFMF 254  
 180 VVFLFAICMAPLNFICGLAVASDPASMPRIPEMLFVASYMAYFNSCLNAIISGYWNN 239  
 255 VVFLFAICMAPLNFICGLAVAINPFAVAPKIDEMLFVLSYMAFYNSCLNAIISGYWNN 314  
 240 FKEEYPRILVLTAVVFVDSSTAVAPVKKPSP 275  
 315 FKEEYPRILVLTAVVFVDSSTAVAPVKKPSP 350

RESULT 11  
 US-08-896-365-9  
 Sequence 9, Application US/08896365

Patent No. 5939264  
 GENERAL INFORMATION:  
 APPLICANT: Rothschild, Max F.  
 APPLICANT: Tuggle, Christopher K.  
 APPLICANT: Messer, Lori A.  
 TITLE OF INVENTION: GENES AND GENETIC MARKERS FOR IMPROVED  
 TITLE OF INVENTION: REPRODUCTIVE TRAITS IN ANIMALS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Zarley, McKee, Thome, Voorhees & Sease  
 STREET: 801 Grand Avenue, Suite 3200  
 CITY: Des Moines  
 STATE: Iowa  
 COUNTRY: USA  
 ZIP: 50309  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/896,365  
 FILING DATE: 18-JUL-1997

CLASSIFICATION: 435  
PRIOR APPLICATION DATA: US 6,570,002, 1,800  
APPLICATION NUMBER: 19-JUL-1996  
FILING DATE: 19-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Nebel, Heidi S.  
REGISTRATION NUMBER: 37,719  
REFERENCE/DOCKET NUMBER: 1591F 021591  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 515-288-3667  
TELEFAX: 515-288-1338  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 153 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Sus scrofa  
CELL TYPE: Melanocyte  
US-08-896-365-9

Query Match 43.88; Score 663.5; DB 2; Length 153;  
Best Local Similarity 81.78; Pred No 1,4e-51;  
Matches 125; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

55 YVYHSKSKKCYVESKSKSYVGLTWIT-NAVLPMIPRGTQVSPRIYSCFPAQSVSS 123  
||||| 123 YVYHSKSKKCYVESKSKSYVGLTWIT-NAVLPMIPRGTQVSPRIYSCFPAQSVSS 60  
DB 1 YVYHSKSKKCYVESKSKSYVGLTWIT-NAVLPMIPRGTQVSPRIYSCFPAQSVSS 60

QY 124 AVTAVVVFHFLVPMIYIPYLRITWITVLOVQVPRDGRPKRKPDPFNTFMVFEV 163  
||||| 124 AVTAVVVFHFLVPMIYIPYLRITWITVLOVQVPRDGRPKRKPDPFNTFMVFEV 120

DB 6 AVTAVVVFHFLVPMIYIPYLRITWITVLOVQVPRDGRPKRKPDPFNTFMVFEV 120

QY 184 LFAICMAPLNFGLAVASDPASVRIPEMIFV 216  
||||| 184 LFAICMAPLNFGLAVASDPASVRIPEMIFV 153  
DB 121 LFAICMAPLNFGLAVASDPASVRIPEMIFV 153

RESULT 12  
US-08-513-974B-344  
Sequence 344, Application US/08513974B  
Patent No 6114139

GENERAL INFORMATION:  
APPLICANT: Hinuma, Shuji  
APPLICANT: Hosoya, Masaki  
APPLICANT: Fujii, Ryo  
APPLICANT: Ohtaki, Tatsuya  
APPLICANT: Fukusumi, Shoji  
APPLICANT: Ohgi, Kazuhiko  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
TITLE OF INVENTION: PRODUCTION AND USE THEREOF  
NUMBER OF SEQUENCES: 360  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CRISHMAN, LLP  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 15-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-324611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 344:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 351 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-513-974B-344

Query Match 18.88; Score 285; DB 3; Length 351;  
Best Local Similarity 26.38; Pred. No. 7.2e-18;  
Matches 76; Conservative 62; Mismatches 129; Indels 22; Gaps 6;

QY 2 NIFVSLAVADLVAVIYPPYLVMSIFNNQWNTGLVQVSGFIMGSLVIGSIFNTGIA 61  
||||| 2 NIFVSLAVADLVAVIYPPYLVMSIFNNQWNTGLVQVSGFIMGSLVIGSIFNTGIA 130

DB 71 NIFVSLAVADLVAVIYPPYLVMSIFNNQWNTGLVQVSGFIMGSLVIGSIFNTGIA 130

QY 62 INRYCYSLKCEKLYSKSKSYVGLTWIT-NAVLPMIPRGTQVSPRIYSCFPAQSV 121  
||||| 62 INRYCYSLKCEKLYSKSKSYVGLTWIT-NAVLPMIPRGTQVSPRIYSCFPAQSV 190

DB 131 VDKYVAVIHSPPSSILPVSNNALGLGCCIMASIPAVYHOGDLHPHPSASNOTFQEW 190

QY 122 -----SSAVTAVVVFHFLVPMIYIPYLRITWITVLOVQVPRDGRPKRKPDPFNTFMVFEV 175  
||||| 122 -----SSAVTAVVVFHFLVPMIYIPYLRITWITVLOVQVPRDGRPKRKPDPFNTFMVFEV 246

DB 191 WPDPRRKRKAVVCTFVFCYLLPLLLIFCYAVV-----LNLKRLK-LNRSKSEAKSKKTA 246

QY 176 VMEVVFVFLAICMAPLNFGLAVASDPASVRIPEMIFVAVSYWYVNSCLNA 230  
||||| 176 VMEVVFVFLAICMAPLNFGLAVASDPASVRIPEMIFVAVSYWYVNSCLNA 300

DB 247 QTVLVVVVVGIGMLPHHILHMAEGVPLTPASFDPRI-----TACLAYNSNSVNP 300

QY 231 IISQWQNFKEKESFRIYSLVTAVPFVDSNDVADSVKPKPSPLMTN 279  
||||| 231 IISQWQNFKEKESFRIYSLVTAVPFVDSNDVADSVKPKPSPLMTN 348

DB 301 IIVAFLENNFRKAVKOVFKCHIKDSHLSDTKEN-KSRIDTPPSINCTH 348

RESULT 13  
 US-08-513-974B-343  
 Sequence 343, Application US/08513974B  
 Patent No. 6114139  
 GENERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Masaki  
 APPLICANT: Fujii, Kyo  
 APPLICANT: Ohtaki, Tetsuya  
 APPLICANT: Fukusumi, Shoji  
 APPLICANT: Ohai, Kazuhito  
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 380  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/513,974B  
 FILING DATE: 14-SEP-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP95/01599  
 FILING DATE: 10-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-093989  
 FILING DATE: 19-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-057186  
 FILING DATE: 16-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-007177  
 FILING DATE: 20-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-326611  
 FILING DATE: 28-DEC-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-270017  
 FILING DATE: 02-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236357  
 FILING DATE: 10-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236156  
 FILING DATE: 10-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189274  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resulov, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/WORK KEY NUMBER: 45763  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 INFORMATION FOR SEQ ID NO: 343:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 349 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 topology: linear  
 MOLECULE TYPE: peptide  
 US-08-513-974B-343  
 Query Match 18.6%, Score 281, DB 3, Length 349,  
 Percent Similarity 26.8%, Pred No. 1,6e-17,  
 Matches 70; Conservative 58; Mismatches 103; Indels 30; Gaps 6;  
 DB 2 NIFVSLAVADLVVAIVYPIVLMSTFNNMNLGYSGLHQVSGFLMGLSVGISINII61A 61  
 DB 71 NFIINTSLATLAVLLEFPFGATVVAITPVAIAFIKFTIHPFTVSMIVSIFTAAMS 130  
 DB 62 IIRVYVICHSLKQIKIVSSKNSICVLLIILLIAVLPLNLPSTIQVFPRIYSGTFAOSV 121  
 DB 131 VDPVVAIVHSPSSSLPVSPNALCGSFIMALSTAM-----ASPVVAHQPIFPDPSQTF 185  
 DB 122 -----SSAVTIAVAVVHFVPMIVFCYLPIMVILVQVGVKPKPKPKPKPHD 171  
 DB 196 QW 241  
 DB 172 ENEVITMVEVYELFAICAPLNFISL.....AVASTFASWVPIPEWLFVASTYMAIFNS 226  
 DB 242 KVTQAVLVVVVVVFQISWIFPHVVRHMAEPYAPPLTATSPFFPI-----TADCLAVSNS 295  
 DB 227 GINATISGVWQNPFFPEPPI 247  
 DB 296 VNPPIIVAFLESNFRKAKQV 316  
 RESULT 14  
 US-08-513-974B-46  
 Sequence 46, Application US/08513974B  
 Patent No. 6114139  
 GENERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Masaki  
 APPLICANT: Fujii, Kyo  
 APPLICANT: Ohtaki, Tetsuya  
 APPLICANT: Fukusumi, Shoji  
 APPLICANT: Ohai, Kazuhito  
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 380  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/513,974B  
 FILING DATE: 14-SEP-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP95/01599  
 FILING DATE: 10-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-093989  
 FILING DATE: 19-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-057186  
 FILING DATE: 16-MAR-1995



PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-007177  
 FILING DATE: 20-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-326611  
 FILING DATE: 28-DEC-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-270017  
 FILING DATE: 02-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236357  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236356  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189274  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 INFORMATION FOR SEQ. ID NO: 46:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 348 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-03-513-974B-4b

Query Match 18.4% Score 279: DB 3: Length 348:  
 Best Local Similarity 26 aa: Pctg No 2 4e-17:  
 Matches 70: Conservative 58: Mismatches 103: Indels 30: Gaps 0:  
 QY 2 NIFVSLAVADVVAIYPPVLVMSIFNMGWNLGILHCOVSGFLMGLSVIGSIFNITGLA 61  
 DB 71 NIFNLISLADLAVLFFLPQATVYALPTWVLSAFICKFIHYFTVSMVLSIFTLAMS 130  
 QY 62 INPVGYTHSLKCKOKLYSSKSLCYLLIMLTAAVLPNLRGTLOVEPRIYCTFAQSV 121  
 DB 131 VDRVAIVHSRPSSSLRVSRNLLGVGFIWLSIAM-----ASVVAIHQRLFRHDSNOTF 185  
 QY 122 -----SSAYTIAAVVEHFLPMITVFCYLRIMILVLPVQPVKPDPRKRLPHD 171  
 DB 186 CNEQPNKLRKAAVYVCFEYLLPILLICGVAKV---LNHLHKLLK-NMSKRSASK 241  
 QY 172 FSEVITVEVYVLFATQWAPLPFTGI-----AVASDPASMPRIPEMLFVASVYMWENS 226  
 DB 212 KRTAQVVLVYVYVFCISWLPFHHVHLMAREGAPLITPASFFPRI-----TARCLANSNS 295  
 QY 227 CLNATISGYMNQNEFFRYRI 247  
 DB 296 SVNPITIAFLSENPRKAYKOV 316

RESULT 15  
 US-08-513-974B-342  
 Sequence 342, Application US/0851974B  
 Patent No. 6114139  
 GENERAL INFORMATION:  
 APPLICANT: Hinuma, Shuji  
 APPLICANT: Hosoya, Masaki

APPLICANT: Fujii, Ryo  
 APPLICANT: Ohnaki, Tetsuya  
 APPLICANT: Fukusumi, Shoji  
 APPLICANT: Ohgi, Kazuhito  
 TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,  
 TITLE OF INVENTION: PRODUCTION, AND USE THEREOF  
 NUMBER OF SEQUENCES: 380  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: DIKE, PRONSTEIN, ROBERTS & CUSHMAN, LLP  
 STREET: 130 Water Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: USA  
 ZIP: 02109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/513, 974B  
 FILING DATE: 14-SEP-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP95/01599  
 FILING DATE: 10-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-093989  
 FILING DATE: 19-AUG-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-057186  
 FILING DATE: 16-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-007177  
 FILING DATE: 20-JAN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-326611  
 FILING DATE: 28-DEC-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-270017  
 FILING DATE: 02-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236357  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-236356  
 FILING DATE: 30-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189274  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189273  
 FILING DATE: 11-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-189272  
 FILING DATE: 11-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Resnick, David S.  
 REGISTRATION NUMBER: 34,235  
 REFERENCE/DOCKET NUMBER: 45753  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617-523-3400  
 TELEFAX: 617-523-6440  
 INFORMATION FOR SEQ. ID NO: 342:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 348 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-513-974B-342

Query Match 18.4% Score 279: DB 3: Length 348:



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 18, 2001, 14:36:41; Search time 63.36 Sec; 309.127 Million cell updates/sec  
(without alignments)

Title: US-09-226-046-6

Perfect score: 1514

Sequence: 1 GNIFVSLAVADLVVAITYP ... VKKKPSPLMTNNNVVYDSV 288

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1443.5	95.3	350	2 138848	Mel-1a melatonin r
2	1241.5	82.0	366	2 146469	Mel-1a melatonin r
3	1070.5	70.7	389	2 872554	Mel-1c receptor su
4	1059.5	70.0	420	2 151666	Mel-1b-melatonin r
5	889.5	58.8	362	2 138930	Melatonin receptor
6	740.5	48.9	613	2 870520	Melatonin receptor
7	730.5	44.2	156	2 144458	Melatonin receptor
8	717.5	47.4	156	2 162107	Melatonin receptor
9	285	18.8	349	2 159316	Melatonin receptor
10	260	17.2	398	2 165517	Melatonin receptor
11	258.5	17.1	398	2 165510	Melatonin receptor
12	258	17.0	394	2 167209	Melatonin receptor
13	258	17.0	398	2 165504	Melatonin receptor
14	257.5	17.0	400	2 165553	Melatonin receptor
15	255.5	16.9	392	2 165535	Melatonin receptor
16	252	16.6	370	2 152315	Melatonin receptor
17	251.5	16.6	455	2 115622	Melatonin receptor
18	247.5	16.3	416	2 130946	Melatonin receptor
19	244.5	16.1	400	2 832804	Melatonin receptor
20	243	16.1	483	2 165896	Melatonin receptor
21	240.5	15.9	412	2 165876	Melatonin receptor
22	240.5	15.9	429	2 165876	Melatonin receptor
23	239.5	15.8	400	2 165876	Melatonin receptor
24	238.5	15.7	405	2 165876	Melatonin receptor
25	237.5	15.7	400	2 165876	Melatonin receptor
26	237.5	15.7	519	2 165876	Melatonin receptor
27	235.5	15.6	670	2 165876	Melatonin receptor
28	234.5	15.5	422	2 165876	Melatonin receptor
29	234	15.5	287	2 165876	Melatonin receptor

30	233.5	15.4	384	2 145490	neuropeptide Y/pep
31	233.5	15.4	418	2 145490	neuropeptide Y/pep
32	232	15.3	515	2 145490	neuropeptide Y/pep
33	231.5	15.3	364	2 145490	neuropeptide Y/pep
34	231.5	15.3	364	2 145490	neuropeptide Y/pep
35	230.5	15.2	380	2 145490	neuropeptide Y/pep
36	230.5	15.2	380	2 145490	neuropeptide Y/pep
37	230	15.2	380	2 145490	neuropeptide Y/pep
38	230	15.2	380	2 145490	neuropeptide Y/pep
39	230	15.2	380	2 145490	neuropeptide Y/pep
40	229.5	15.1	355	2 145490	neuropeptide Y/pep
41	228	15.1	347	2 145490	neuropeptide Y/pep
42	227.5	15.0	319	2 145490	neuropeptide Y/pep
43	227.5	15.0	319	2 145490	neuropeptide Y/pep
44	227.5	15.0	319	2 145490	neuropeptide Y/pep
45	227.5	15.0	412	2 145490	neuropeptide Y/pep

## ALIGNMENTS

RESULT 1  
138848  
Mel-1a melatonin receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence-revision 29-May-1998 #text-change 20-Apr-2000  
C:Accession: 138848  
R:Reppert, S.M.; Weaver, D.R.; Ebisawa, T.  
Neuron 13, 1177-1185, 1994  
A:Title: Cloning and characterization of a mammalian melatonin receptor that mediates  
A:Reference number: 138848; NCID:95033233  
A:Accession: 138848  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-350 <RES>  
A:Cross-references: EMBL:014108, NID:9602129, FICN:AAH17729 1; PIR:G602130  
C:Superfamily: vertebrate rhodopsin

Query Match 95.3%; Score 1443.5; DB 2; Length 350;  
Best Local Similarity 96.9%; Pred. 3.9e-120;  
Matches 280; Conservative 1; Mismatches 74; Indels 1; Gaps 1;  
DB 1 GNIFVSLAVADLVVAITYPPLVMSIFNNGWMDGYLHCQVSGFLMGSLVIGSIFNTG 60  
DB 62 GNIFVSLAVADLVVAITYPPLVMSIFNNGWMDGYLHCQVSGFLMGSLVIGSIFNTG 121  
UY 61 AINRYCICSLKCDKLYSSKNSLCYLLIMLT-AAVLPRLPRTIQLYPRYSCTFAQ 119  
DB 122 AINRYCICSLKCDKLYSSKNSLCYLLIMLT-AAVLPRLPRTIQLYPRYSCTFAQ 181  
UY 120 SVSSAVTAAVVFHFLVMIIVFCYLLIMLTAAVLPRLPRTIQLYPRYSCTFAQ 179  
DB 182 SVSSAVTAAVVFHFLVMIIVFCYLLIMLTAAVLPRLPRTIQLYPRYSCTFAQ 241  
UY 180 VVFLPACIAPLNTICLAVASDPASVPPPELFAVASYMAVFNCLAAITSCYNNQ 239  
DB 242 VVFLPACIAPLNTICLAVASDPASVPPPELFAVASYMAVFNCLAAITSCYNNQ 301  
UY 240 PRKRYPIIVSIVTARFVFNSSNVADRYKWRKPSFLMTNNNVYKDSV 288  
DB 302 PRKRYPIIVSIVTARFVFNSSNVADRYKWRKPSFLMTNNNVYKDSV 350

RESULT 2  
146459  
Mel-1a melatonin receptor - sheep  
C:Species: Ovis orientalis aries, Ovis ammon aries (Jamaica sheep)  
C:Date: 19-Dec-1997 #sequence-revision 19-Dec-1997 #text-change 17-Mar-2000  
C:Accession: 146459  
R:Reppert, S.M.; Weaver, D.R.; Ebisawa, T.  
Neuron 13, 1177-1185, 1994  
A:Title: Cloning and characterization of a mammalian melatonin receptor that mediates







```

QY 121 VSSAV-----TIAVVFHFLVPMITVFCYLRIMVLVQVQPVKDDPKRIKPHDFRNF 175
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 223 HPTWVWENLTKICETIFAFIFLITIVCY---GIMILPLKS--VPMLSGSKEDNLPRI 278
QY 176 VTM-FVVFVFLATGAPLNFITGLAVASDPASMPRIPEMF-VASYX---MAYFNSCN 229
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 279 TRMLVVAVAVICWTPHIVIIKA-----LITPETTFQVSWHFCALGYTNSCLN 332
QY 220 AIISSYWNQNFKEKFPYPIVSLVTAPEFVDSNVADPVKWPSPMLTNNV 282
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 333 PVLAFLDENKRCRCEEFICP--TSSTIEQNSITPRQNTREPS--TANTV 380

RESULT 11
A57510
C:Species: Mus musculus (house mouse)
C:Date: 08-Dec-1995 #sequence-revision 08-Dec-1995 #text-change 24-Nov-1999
C:Accession: A57510: 148665: 566513: 149300
R:Kautman, D.L., Reitz, D.E., Antin, P., Jan, J.: Magerl, K.: Newman, D.: Tran, T.
J. Biol. Chem. 270, 15877-15883, 1995
A:Title: Characterization of the murine mu opioid receptor gene.
A:Reference number: A57510: MIM: 45318184
A:Accession: A57510
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-398 <KAU>
A:Cross-references: GR:019380
R:Min, B.H.: Augustin, L.B.: Peisheim, R.F.: Fuchs, J.A.: Loh, H.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 9081-9085, 1994
A:Title: Genomic structure analysis of promoter sequence of a mouse mu opioid receptor
A:Reference number: 148665: MIM: 94377496
A:Accession: 148665
A:Status: translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-398 <RES>
A:Cross-references: EMBL:010561: NID:9555690: PIDD:AA80673.1: FID:955569
R:Ross, J.C.: Fan, Y.X.: Brown, G.P.: Parnham, G.W.
FEBS Lett. 359, 192-196, 1995
A:Title: Antisense mapping the MOR-1 opioid receptor evidence for alternative splicing
A:Reference number: 149300: MIM: 45377399
A:Accession: 149300
A:Status: S66513
A:Status: nucleic acid sequence not shown: translation not shown
A:Molecule type: mRNA
A:Residues: 1-398 <POS>
A:Cross-references: EMBL:026915: NID:91055230: PIDD:AAA9170.1: PFD:91055231
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C:Genetics:
A:Gene: MOR-1
A:Mutations: 95/2: 213/1: 186/3
C:Superfamily: vertebrate rhodopsin
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembran
Query Match 17.1% Score 258.5: DB 2: Length 398:
Best Local Similarity 24.1%: Pred. No. 1.9e-15:
Matches 70: Conservative 67: Mismatches 126: Indels 27: Gaps 10:

```

```

QY 220 AIISSYWNQNFKEKFPYPIVSLVTAPEFVDSNVADPVKWPSPMLTNNV 279
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 333 PVLAFLDENKRCRCEEFICPST-----IDQNSAFITQNTREPSIAN 378

RESULT 12
JC7209
C:Species: Drosophila melanogaster
C:Date: 09-Jun-2000 #sequence-revision 09-Jun-2000 #text-change 12-Apr-2000
C:Accession: JC7209
R:Lenz, C.: Sondergaard, L.: Grimelikhuisen, C.J.P.
Biochem. Biophys. Res. Commun. 269, 91-96, 2000
A:Title: Molecular cloning and genomic organization of a novel receptor from Drosophi
A:Reference number: JC7209: MIM: 20160455
A:Accession: JC7209
A:Molecule type: mRNA
A:Residues: 1-394 <LEN>
A:Cross-references: GR:AF20216
C:Comment: This receptor is a G-protein-coupled receptor and a transmembrane protein
C:Genetics:
A:Map position: X distal end
A:Mutations: 38/2: 161/3: 193/2: 243/3: 267/3: 309/3: 460/3
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
Query Match 17.0% Score 258: DB 2: Length 394:
Best Local Similarity 22.8%: Pred. No. 2.1e-15:
Matches 68: Conservative 69: Mismatches 106: Indels 66: Gaps 12:

```





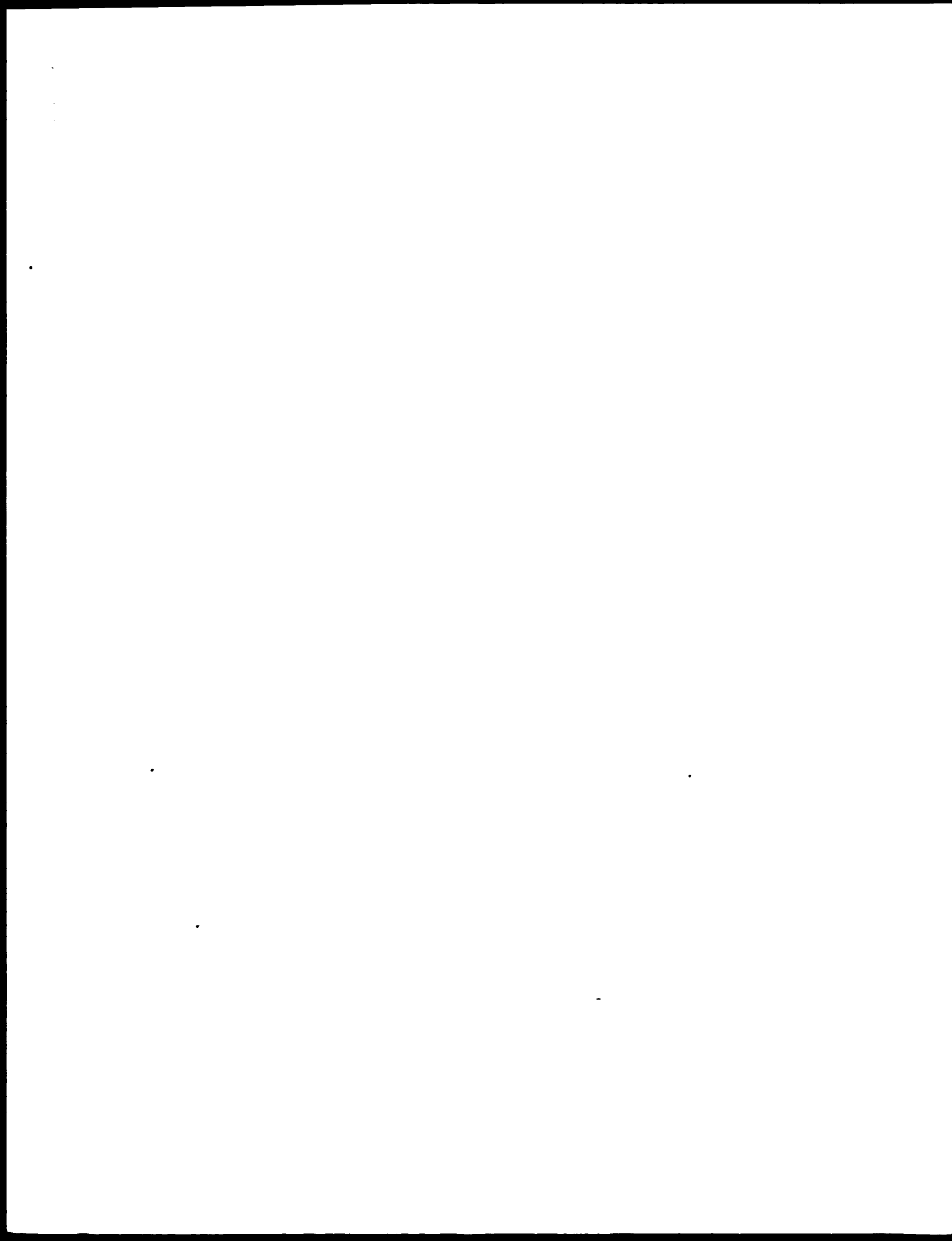
Tue Feb 20 11:43:05 2001

us-09-226-046-6.rpt

Page 7

Db 228 HPIWMENTLKICVFIFAFIMFVLIITVY...GLMILRLKS-VEMLSGSKERQNT PPI 280  
OY 176 VTM-FVAVLPAICWAPLNFGLAVASDPASMPRIPEMLF-VASYX---MAYNSCLN 229  
Db 281 TRMVLVAVAVFVCTPIHIVITKA-----LVTIPETTFQIVSMHFCIALGYTNSCLN 334  
OY 238 AITSGYWNQNPFPKYPPIVSLVTARFFVDSNDVADRVKWKPSPLMTN 279  
Db 335 PVLVAFLDENFKCFRFECPITSSN---IEQONSTRIRONTROHPSTAN 380

Search completed: February 18, 2001, 19:20:53  
Job time: 17052 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 19, 2001, 13:42:23 : Search time 54.38 seconds  
(without alignments)  
171.032 Million cell updates/sec

Title: US-09-226-046-6  
Perfect score: 1514  
Sequence: 1 GNIFVWSLAVDLVLAIPY.....YKWKSPPLMTNNVVKVDSV 288

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 88757 seqs, 32294092 residues  
Total number of hits satisfying chosen parameters: 88757

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1443.5	95.3	350	1	MELIA_HUMAN
2	1312.5	86.7	353	1	MELIA_PIG
3	1308.5	86.4	353	1	MELIA_MOUSE
4	1272.5	84.0	353	1	MELIA_CHICK
5	1241.5	82.0	356	1	MELIA_SHEEP
6	1109.5	73.3	257	1	MELIA_BOVIN
7	1070.5	70.7	289	1	MELIA_CHICK
8	1059.5	70.0	420	1	MELIA_XENLA
9	1058.5	69.9	346	1	MELIA_CHICK
10	883.5	58.8	362	1	MELIA_HUMAN
11	740.5	48.4	613	1	MELIA_HUMAN
12	719.5	47.5	575	1	MELIA_SHEEP
13	717.5	47.4	513	1	MELIA_SHEEP
14	714.5	47.2	593	1	MELIA_RAT
15	667.5	44.1	154	1	MELIA_PIG
16	627.5	41.4	153	1	MELIA_PIG
17	580	38.3	153	1	MELIA_PIG
18	533.5	35.2	152	1	MELIA_PIG
19	532.5	35.2	151	1	MELIA_PIG
20	527.5	34.8	157	1	MELIA_PIG
21	526.5	34.8	153	1	MELIA_PIG
22	460	30.4	120	1	MELIA_PIG
23	348.5	23.0	349	1	MELIA_PIG
24	285	18.5	349	1	MELIA_PIG
25	281	18.4	348	1	MELIA_PIG
26	269.5	17.4	401	1	MELIA_PIG
27	263.5	17.4	401	1	MELIA_PIG
28	260.5	17.2	398	1	MELIA_PIG
29	250.5	17.2	398	1	MELIA_PIG
30	248.5	17.1	400	1	MELIA_PIG
31	247.5	17.0	400	1	MELIA_PIG
32	247.5	17.0	400	1	MELIA_PIG
33	253.5	16.7	499	1	MELIA_PIG

34	252.5	16.7	401	1	OPRM_PIG
35	252	16.6	370	1	OPRM_PIG
36	251.5	16.6	455	1	YKXS_CAEEL
37	244.5	16.1	400	1	B3AR_MOUSE
38	243	16.1	483	1	B3AR_MOUSE
39	240.5	15.9	428	1	B3AR_MOUSE
40	238.5	15.8	405	1	B3AR_MOUSE
41	237.5	15.7	383	1	NYLR_PIG
42	237.5	15.7	400	1	B3AR_PAT
43	237.5	15.7	519	1	TIR2_DROME
44	234.5	15.5	428	1	GCRC_MOUSE
45	234	15.5	368	1	GALR_HUMAN

## ALIGNMENTS

RESULT 1  
ID MELIA\_HUMAN STANDARD. PRT: 350 AA  
AC P48039;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE MELANIN RECEPTOR TYPE 1A (MEL-1A-R).  
GN MTR1A.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-95033233; PubMed-7946354;  
RA REPPERT S.M., Weaver D.R., Ebisawa T.;  
RT Cloning and characterization of a mammalian melatonin receptor that  
RT mediates reproductive and circadian responses.";  
RL Neuron 13:1177-1185(1994).  
RN [2]  
RP SEQUENCE FROM N.A., AND VARIANTS TRP-54 AND VAL-157.  
RC TISSUE-LEUCOCYTE;  
RX MEDLINE-99400459; PubMed-10471411;  
RA Edisawa T., Kajimura N., Uchiyama M., Katoh M., Sakimoto M.,  
RA Watanabe T., Ozeki Y., Ikeda M., Jodo T., Sugishita M., Iwase T.,  
RA Kamel Y., Kim K., Shibui K., Kudo Y., Yanada N., Toyoshima P.,  
RA Okawa M., Takahashi K., Yamuchi T.;  
PT "Allelic variants of human melatonin 1a receptor: function and  
PT prevalence in subjects with circadian rhythm sleep disorders";  
RL Biochem. Biophys. Res. Commun. 262:832-837(1999).  
CC -! FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. LIKELY TO MEDIATES  
CC THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY  
CC OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G  
CC PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.  
CC -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC -! TISSUE SPECIFICITY: EXPRESSED IN HYPOTHALAMIC, PARS TYPICALIS AND  
CC HYPOTHALAMIC SUPRACHIASMATIC NUCLEI (SN). HIPPOCAMPUS.  
CC -! SIMILARITY: BELONGS TO FAMILY OF G-PROTEIN COUPLED RECEPTORS  
CC  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation.  
CC The European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch>)  
CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch).  
CC  
CC EMBL: U14108; AB017720.1;  
CC EMBL: AB029933; EA055403.1;  
CC EMBL: AB029933; BA055403.1;  
CC CCFP: CCFP\_2072;  
CC MIM: 600665;  
CC INTERPRO: IPR000025;  
CC INTERPRO: IPR000276;  
CC INTERPRO: IPR002279;  
CC PFM: PFM00001; Tm1\_1;  
CC



```

DB 185 SVSSAVTIAVAVVHFHIVMIIIVICYLRIWTLVQVPPKPKPDKPQDFRNVTMF 244
DB 180 VVFLVFAICMAPLNLIGLIVASDPASWVFRIPFEMLEFVASYMAYFNSCLNAIISGYWNON 239
DB 245 VVFLVFAICMAPLNLIGLIVASDPATVAPRIPEMLEFVASYMAYFNSCLNAIISGYLNNON 304
DB 240 FRKERYRIIVSLVTRARVFFVDSNDVADRVKPKPPLMTNNVAVKVDV 288
DB 305 FRKERYRIIVSLVTRAKMCFVDSNDVADRVKPKPPLMTNNVAVKVDV 353

RESULT 3
MLA_MOUSE STANDARD: PRT: 353 AA.
ID 061184:
AC 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MELATONIN RECEPTOR TYPE 1A (MEL-1A-R).
GN MTNRIA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C:
RA MEDLINE-96290986; PubMed-8754776;
RA Poca A L., Godson C., Weaver D.R., Reppert S.M.;
RT "Structure, characterization, and expression of the gene encoding the
RT mouse melatonin receptor."
RT Endocrinology 137:3469-3477(1996).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. LIKELY TO MEDIATES
CC THE REPERGNOTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY
CC OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G
CC PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: U52222; AAB08755.1; -
DB GCRDB: GCR_1650; -
DB MGD: MGI:102967; MTNRIA.
DB INTERPRO: IPR000025; -
DB INTERPRO: IPR000176; -
DB INTERPRO: IPR002478; -
DB PFM: PFM0001; 7tm_1; 1.
DB PRINTS: PR00847; MELATONINR.
DB PRINTS: PR01149; MELATONINR.
DB PROSITE: PS00337; G-PROTEIN_RECEP_FL_1; 1
DB PROSITE: PS00362; G-PROTEIN_RECEP_FL_1; 1
DB PROSITE: PS00362; G-PROTEIN_RECEP_FL_1; 1
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 32
FT TRANSMEM 33 53
FT DOMAIN 54 66
FT TRANSMEM 67 87
FT DOMAIN 88 105
FT TRANSMEM 106 126
FT DOMAIN 127 145
FT TRANSMEM 146 166
FT DOMAIN 167 190
FT TRANSMEM 191 211
FT DOMAIN 212 243
FT TRANSMEM 244 264
FT DOMAIN 265 277
FT TRANSMEM 278 298

```

```

FT DOMAIN 299 353 CYTOPLASMIC (POTENTIAL).
FT DISULFID 103 180 BY SIMILARITY.
FT CARBOHYD 4 4 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 10 10 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 353 AA; 39837 MW; 0375C2FD41B54C74 Cpf64;

Query Match 86.4%; Score 1308.5; DB 1: Length 353;
Best Local Similarity 84.4%; Pred. No. 1.5e-83;
Matches 244; Conservative 25; Mismatches 19; Indels 1; Gaps 1;

DB 1 GNFVYSLAVADVVAIYPPYPLVMSIFNNQWNLGYLHCQVSGFLMGLSYGSIENITGI 60
DB 65 GNFVYSLAVADVVAIYPPYPLVMSIFNNQWNLGYLHCQVSAFAMGLSYGSIENITGI 124
DB 61 AINPCYICHSKCDKLYSKNSKSLCYLLIMLLT-AAVLPNRRGLQYEPRIYSCFPAQ 119
DB 125 AANRCYICHSKDKKLYSKNSKSLCYVFLIMLLTAAIMPLNLGLQYDPRYSCFPAQ 184
DB 120 SVSSAVTIAVAVVHFHIVMIIIVICYLRIWTLVQVPPKPKPDKPQDFRNVTMF 179
DB 185 SVSSAVTIAVAVVHFHIVMIIIVICYLRIWTLVQVPPKPKPDKPQDFRNVTMF 244
DB 180 VVFLVFAICMAPLNLIGLIVASDPASWVFRIPFEMLEFVASYMAYFNSCLNAIISGYWNON 239
DB 245 VVFLVFAICMAPLNLIGLIVASDPATVAPRIPEMLEFVASYMAYFNSCLNAIISGYLNNON 304
DB 240 FRKERYRIIVSLVTRARVFFVDSNDVADRVKPKPPLMTNNVAVKVDV 288
DB 305 FRKERYRIIVSLVTRAKMCFVDSNDVADRVKPKPPLMTNNVAVKVDV 353

RESULT 4
MLA_CHICK STANDARD: PRT: 353 AA.
ID 049285:
AC 01-FEB-1996 (Rel. 33, Created)
DI 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 34, Last annotation update)
DE MELATONIN RECEPTOR TYPE 1A (MEL-1A-R) (CKA).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-96073557; PubMed-7576645;
RC Reppert S.M., Weaver D.R., Cassone V.M., Godson C.,
RC Kolakowski L.F. Jr.;
RT "Melatonin receptors are for the birds: molecular analysis of two
RT receptor subtypes differentially expressed in chick brain."
RT Neuron 15:1003-1015(1995).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTEINS
CC THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN OPTIC TECTUM AND RETINA. LESS IN
CC NESTITATUM, AHYPOTHALAMUS AND THALAMUS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL: U31820; AAA92498.1; -
DB GCRDB: GCR_1081; -
DB INTERPRO: IPR000025; -
DB INTERPRO: IPR003276; -
DB INTERPRO: IPR003278; -

```

DR PFAM: PF00001:7tm1.1  
 DR PRINTS: PR00217: GPCRPHODPSN  
 DR PRINTS: PR00857: MELATONINR  
 DR PRINTS: PR01149: MELATONINR  
 DR PROSITE: PS00237: G-PROTEIN\_RECEP\_FL1\_1  
 DR PROSITE: PS00262: G-PROTEIN\_RECEP\_FL2\_1  
 RT G-protein coupled receptor: transmembrane; glycoprotein.  
 RT Mel 1a melatonin receptor.  
 RT Mel 1a melatonin receptor.  
 RT Biochim. Biophys. Acta 1356:299-307(1997).  
 CC FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. LIKELY TO MEDIATES  
 CC THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY  
 CC OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G  
 CC PROTEIN THAT INHIBITS ADENYLYL CYCLASE ACTIVITY.  
 CC SURCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL: U14109: AAB17721.1  
 DR EMBL: AF045319: AAC92699.1  
 DR HSSP: P29274: 1MMH  
 DR GCRDB: GCR1583:  
 DR INTERPRO: IPR00925:  
 DR INTERPRO: IPR00276:  
 DR INTERPRO: IPR00278:  
 DR PFAM: PF00001: 7tm1.1: 1.  
 DR PRINTS: PR00857: MELATONINR  
 DR PRINTS: PR01149: MELATONINR  
 DR PROSITE: PS00237: G-PROTEIN\_RECEP\_FL1\_1  
 DR PROSITE: PS00262: G-PROTEIN\_RECEP\_FL2\_1  
 KW G-protein coupled receptor; transmembrane; glycoprotein; polymorphism.  
 FT DOMAIN 1 45  
 FT TRANSMEM 45 56  
 FT DOMAIN 67 79  
 FT TRANSMEM 80 100  
 FT DOMAIN 101 118  
 FT TRANSMEM 119 139  
 FT DOMAIN 140 158  
 FT TRANSMEM 159 179  
 FT DOMAIN 180 203  
 FT TRANSMEM 204 224  
 FT DOMAIN 225 236  
 FT TRANSMEM 237 277  
 FT DOMAIN 278 290  
 FT TRANSMEM 291 311  
 FT DOMAIN 312 366  
 FT DISULFID 116 193  
 FT CARBOHYD 15 16  
 FT CARBOHYD 23 23  
 FT VARIANT 282 282  
 FT VARIANT 358 358  
 FT VARIANT 361 361  
 SU SEQUENCE 366 AA: 40400 MW: 5386ED0DF9710E4A CRC64:

Query Match 84.0% Score 1272.5; DB 1: Length 353;  
 Best Local Similarity 81.3%; Pred. No. 4 3e-81;  
 Matches 235; Conservative 29; Mismatches 24; Indels 1; Gaps 1;

DR 1 GNIFVSLAVADLVVAIYPPYPLVMSIFNNKNGVLSGFLMGLSVISGIFNIGI 60  
 DR 65 GNIFVSLAVADLVVAIYPPYPLVMSIFNNKNGVLSGFLMGLSVISGIFNIGI 124  
 DR 61 AINRCYICHSKCKDKLYSSKNSLCYVLLIMLT-AAVPLNLRGTLQYEPRIYSCFEAQ 119  
 DR 125 AINRCYICHSKCKDKLYSSKNSLCYVLLIMLT-AAVPLNLRGTLQYEPRIYSCFEAQ 184  
 QY 120 SVSASATIAVVFHFLVPMIYIFCYLPRLWILVAVQGVKDKRDKPKLPHDFRFTMF 179  
 DB 185 SVSASATIAVVFHFLVPMIYIFCYLPRLWILVAVQGVKDKRDKPKLPHDFRFTMF 244  
 QY 1180 VVVFVFAICWALNFGVLAVASDPASVPRIPFEMLFVASYAYVNSCLNATISYKMNON 239  
 DB 245 VVVFVFAICWALNFGVLAVASDPASVPRIPFEMLFVASYAYVNSCLNATISYKMNON 304  
 QY 240 PRKEYRRIIVSLVAVVFVDSGSDVADRVKWPSPPLMTNNNVKVDV 288  
 DB 305 PRKEYRRIIVSLVAVVFVDSGSDVADRVKWPSPPLMTNNNVKVDV 353  
 RESULT 5  
 ML1A\_SHEEP STANDARD: PRT: 366 AA  
 AC P48040: 046608:  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE MELATONIN RECEPTOR TYPE 1A (MEL-1A-R).  
 GN MTNP1A  
 OS Ovis aries (Sheep).  
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 OC Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae:  
 OC Bovidae: Caprinae: Ovis.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PILOTARY PARS TUBERIALIS;  
 RX MEDLINE=95033333; PubMed=7946354;  
 RA Reppert S.M., Weaver D.R., Ebisawa T.  
 RT "Cloning and characterization of a mammalian melatonin receptor that  
 RT mediates reproductive and circadian responses."

RL Neuron 13:1177-1185(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97337902; PubMed=9194573;  
 RA Partridge P., Conway S., Jockers R., Strosberg A.D.,  
 RA Garabito-Lemaitre B., Delarange P., Morgan P.J.  
 RT Cloning and functional analysis of a polymorphic variant of the ovine  
 RT Mel 1a melatonin receptor.  
 RT Biochim. Biophys. Acta 1356:299-307(1997).  
 CC FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. LIKELY TO MEDIATES  
 CC THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY  
 CC OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G  
 CC PROTEIN THAT INHIBITS ADENYLYL CYCLASE ACTIVITY.  
 CC SURCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL: U14109: AAB17721.1  
 DR EMBL: AF045319: AAC92699.1  
 DR HSSP: P29274: 1MMH  
 DR GCRDB: GCR1583:  
 DR INTERPRO: IPR00925:  
 DR INTERPRO: IPR00276:  
 DR INTERPRO: IPR00278:  
 DR PFAM: PF00001: 7tm1.1: 1.  
 DR PRINTS: PR00857: MELATONINR  
 DR PRINTS: PR01149: MELATONINR  
 DR PROSITE: PS00237: G-PROTEIN\_RECEP\_FL1\_1  
 DR PROSITE: PS00262: G-PROTEIN\_RECEP\_FL2\_1  
 KW G-protein coupled receptor; transmembrane; glycoprotein; polymorphism.  
 FT DOMAIN 1 45  
 FT TRANSMEM 45 56  
 FT DOMAIN 67 79  
 FT TRANSMEM 80 100  
 FT DOMAIN 101 118  
 FT TRANSMEM 119 139  
 FT DOMAIN 140 158  
 FT TRANSMEM 159 179  
 FT DOMAIN 180 203  
 FT TRANSMEM 204 224  
 FT DOMAIN 225 236  
 FT TRANSMEM 237 277  
 FT DOMAIN 278 290  
 FT TRANSMEM 291 311  
 FT DOMAIN 312 366  
 FT DISULFID 116 193  
 FT CARBOHYD 15 16  
 FT CARBOHYD 23 23  
 FT VARIANT 282 282  
 FT VARIANT 358 358  
 FT VARIANT 361 361  
 SU SEQUENCE 366 AA: 40400 MW: 5386ED0DF9710E4A CRC64:

Query Match 82.0% Score 1241.5; DB 1: Length 365;  
 Best Local Similarity 80.6%; Pred. No. 6e-79;  
 Matches 233; Conservative 25; Mismatches 30; Indels 1; Gaps 1;  
 QY 1 GNIFVSLAVADLVVAIYPPYPLVMSIFNNKNGVLSGFLMGLSVISGIFNIGI 60  
 DB 78 GNIFVSLAVADLVVAIYPPYPLVMSIFNNKNGVLSGFLMGLSVISGIFNIGI 137  
 QY 61 AINRCYICHSKCKDKLYSSKNSLCYVLLIMLT-AAVPLNLRGTLQYEPRIYSCFEAQ 119  
 DB 138 AINRCYICHSKCKDKLYSSKNSLCYVLLIMLT-AAVPLNLRGTLQYEPRIYSCFEAQ 197

```

QY 120 SVSASATIAVAVHFLVPMILVIFCYLRIMVLYGVORVKKPKRKLPHDFRNFVIMF 179
DB 198 SVSSATYIAVAVHFLVPMILVIFCYLRIMVLYGVORVKKPKRKLPHDFRNFVIMF 257
QY 180 VVEFLFAICMAPLNFILGLVAVSDPAPRIPPELVEVASYMAVFNSCLNAILISGVWNN 239
DB 258 VVEFLFAICMAPLNFILGLVAVSDPAPRIPPELVEVASYMAVFNSCLNAILISGVWNN 317
QY 240 FRKEKRIIVSLVAVAFVNDSSNDVADRVKMKRPSPLMTNNVAVKDVSV 288
DB 318 FRKEKRIIVSLVAVAFVNDSSNDVADRVKMKRPSPLMTNNVAVKDVSV 365

RESULT 5
MLIA_BOVIN STANDARD: PRT: 257 AA
ID MLIA_BOVIN
AC 002769
DT 15-JUL-1998 (Rel. 36, Created)
DI 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE MELATONIN RECEPTOR TYPE 1A (MEL-1A-R) (FRAGMENT).
CN MTNRIA
OS Bos taurus (Bovine).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HYPOTHALAMUS, AND PITUITARY;
RX MEDLINE=97262109; PubMed=9107687;
RA Messer L.A., Wang L., Tsigile C.K., Verle M., Chardon P., Pomp D.,
RA Womack J.E., Barendse W., Crawford A.M., Notter D.R.,
RA Rothchild M.F.;
RT Mapping of the melatonin receptor 1a (MTNRIA) gene in pigs, sheep,
RT and cattle.
RL Mamm. Genome 8:368-370(1997).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN, LIKELY TO MEDIATES
CC THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY
CC OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G
CC PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U73327; AAC48725.1;
CC GCRDB: GCR_1163;
CC INTERPRO: IPR000276;
CC PFAM: PF00001; 7tm.1; 1.
CC PROSITE: PS00237; G-PROTEIN_RECEP_F1.1; 1.
CC PROSITE: PS50262; G-PROTEIN_RECEP_F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC
CC NON_TER 1
CC DOMAIN 1
CC TRASMEM 23
CC DOMAIN 22
CC TRASMEM 5
CC DOMAIN 43
CC TRASMEM 64
CC DOMAIN 85
CC TRASMEM 107
CC DOMAIN 128
CC TRASMEM 160
CC DOMAIN 181
CC TRASMEM 194
CC TRASMEM 215
CC TRASMEM 216
CC TRASMEM 220
CC TRASMEM 257
CC NON_TER 257
CC SPODENCE 257 AA: 29370 MW: DQ9A675FE75ADE03 CRC54:

```

```

Query Match 73.3%; Score 1109.5; DB 1; Length 257;
Best Local Similarity 81.3%; Pred No. 5.4e-70;
Matches 209; Conservative 19; Mismatches 28; Indels 1; Gaps 1;

QY 20 YPLVMSIFPNNGLVGLHGVSGFLMSLSVIGSFRTITGTAIRRYCYCHSKDKPKYS 79
DB 1 YPLALAVINDGSLSLHCOLSGFLMGLSVIGSVNIGTAIRNRYCCCHSKRYNKLKS 60
QY 80 SKNSLCVLLMLLT-AAVPLNRGTLQEPRIYSCFPAQSSAYTLAVVHFLVPM 138
DB 61 STNSLCVFLMLLTVAIVPNCVSTLOYDPRITSCITQSSAYTLAVVHFLVPM 120
QY 139 IIVFCYLRIMVLYGVORVKKPKRKLPHDFRNFVIMFVYVFLACMAPLNFILGLV 198
DB 121 LVIFCYLRIMVLYGVPMVRYKPKRKLPHDFRNFVIMFVFLACMAPLNFILGLV 180
QY 199 VASDPASVAPRIPPELVEVASYMAVFNSCLNAILISGVWNNFRKEKRIIVSLVAVAF 258
DB 181 VASDPASVAPRIPPELVEVASYMAVFNSCLNAILISGVWNNFRKEKRIIVSLVAVAF 240
QY 259 VDSSNDVADRVKMKRPS 275
DB 241 VDSSNHVAFPIKRPSP 257

RESULT 7
MLIR_CHICK STANDARD: PRT: 289 AA
ID MLIR_CHICK
AC P10500;
DT 01-OCT-1996 (Rel. 34, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE MELATONIN RECEPTOR TYPE 1B (MEL-1B-R) (FRAGMENT).
CN Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=96063731; PubMed=7289552;
RA Liu F., Yuan H., Sugamori K.S., Hamadanizadeh A., Lee F.J.S.,
RA Pang S.F., Brown G.M., Pristupa Z.B., Niznik H.B.;
RT Molecular and functional characterization of a partial cDNA encoding
RT a novel chicken brain melatonin receptor.
RL FEBS Lett. 374:273-278(1995).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTEINS
CC THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN AND KIDNEY WITH TRACE LEVELS IN LUNGS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U30609; AAA85098.1;
CC GCRDB: GCR_1082;
CC INTERPRO: IPR00276;
CC PFAM: PF00001; 7tm.1; 1.
CC PROSITE: PS00237; G-PROTEIN_RECEP_F1.1; 1.
CC PROSITE: PS50262; G-PROTEIN_RECEP_F1.2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein.
CC
CC NON_TER 1
CC DOMAIN 1
CC TRASMEM 23
CC DOMAIN 43
CC TRASMEM 64
CC TRASMEM 107
CC TRASMEM 128
CC TRASMEM 160
CC TRASMEM 181
CC TRASMEM 194
CC TRASMEM 215
CC TRASMEM 216
CC TRASMEM 220
CC TRASMEM 257
CC NON_TER 257
CC CYTOPLASMIC (POTENTIAL).

```









MEDLINE-98415731: PubMed-9744482:  
 Drew J.E., Sarrett P., Williams I.M., Conway S., Morgan P.J.:  
 "The ovine melatonin-related receptor: cloning and preliminary  
 distribution and binding studies."  
 J. Neuroendocrinol. 10:651-661(1998).  
 [2]  
 SEQUENCE OF 128-245 FROM N.A.  
 MEDLINE-96228068: PubMed-8647286:  
 Reppert S.M., Weaver D.P., Ebisawa T., Mahle C.D.:  
 "Cloning of a melatonin-related receptor from human pituitary."  
 Kolakowski L.F. Jr.  
 FEBS Lett. 386:219-224(1996).  
 -1- FUNCTION: DOES NOT BIND MELATONIN (BY SIMILARITY).  
 -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb.slb.ch/announce/>  
 or send an email to [license@isb.slb.ch](mailto:license@isb.slb.ch)).  
 EMBL: AF047829; AAC04275.1;  
 EMBL: U52221; AAC48609.1;  
 INTERPRO: IPR000276;  
 PFM: PFO0001; 7tm\_1; 1.  
 PRINTS: PR01151; MELATONINR.  
 PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_1; 1  
 PROSITE: PS0262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 G-protein coupled receptor. Transmembrane.  
 DOMAIN 1 30  
 1 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 2 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 3 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 4 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 5 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 6 (POTENTIAL).  
 EXTRACELLULAR (POTENTIAL).  
 7 (POTENTIAL).  
 CYTOPLASMIC (POTENTIAL).  
 BY SIMILARITY.  
 R -> L (IN REF. 2).  
 L -> M (IN REF. 2).  
 APD -> D (IN REF. 2).  
 CONFLICT 158 158  
 CONFLICT 218 220  
 SEQUENCE 575 AA: 62803 MW: E2CAIC11FEEDFE8 CRG44;  
 47.5% Score 719.5; DB 1; Length 575;  
 Best Local Similarity 48.1%; Pred. No. 6,7e-43;  
 Matches 129: Conservative 62; Mismatches 74; Indels 3; Gaps 2;  
 1 GNIFVSLAVADLVVAIVYPLVMSIFNNKNGLYHCQVSGFLMGSLVSSIFNITGI 60  
 63 GNFFVSLVADMLVAIVYPLMLHAMAIGMDKSLDQGMGFTIGSLVSGSIFNIMAI 122  
 61 AIRRYGICSLKCDKLYSSKNSLCVLLIMLTLA-VLPLNLRGSLQYPRYSCTFAQ 119  
 123 AIRRYGICSLQYERFYSFRNTGICLVATWIMTVLAVLPNMYIGIIEDEPTVICIN 182  
 120 SVSSAVTIAVVEFLVPMITIVFCYLRITWILVLOVPQVKKPDKRKLPHDFRNV 179  
 183 VNNAPAVITVICIFVPLIVGFCYVKKITWYKLAARD--PAGQNDNDQJAEVRF 240  
 180 VVFLVLCAPLNFIGLVAASDPASVPRIPMLFVASIYMAVFNSCINAIISGYW 239

DB 241 VIFLLAVCMCPINALTVLVAVNPKEKAKRIPMWVLAFLAFVNSCLNAVITGVLEN 300  
 QY 240 FRKEYPPVLSVATPAVFVFDSSNDVAD 267  
 DB 301 FRREYWTIFHAKRPVFLSGLLTDVRE 328  
 RESULT 13  
 MLIA-RAT STANDARD; PRT: 156 AA.  
 ID MLIA-RAT  
 AC P49218;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DI 01-FEB-1996 (Rel. 33, Last sequence update)  
 DR 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE MELATONIN RECEPTOR TYPE 1A (MEL-1A-P) (FRAGMENT).  
 GN MTNRLA.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-HYPOTHALAMUS, AND PITUITARY;  
 RX MEDLINE-95033233; PubMed-7946354;  
 RA Reppert S.M., Weaver D.P., Ebisawa T.;  
 RT Cloning and characterization of a mammalian melatonin receptor that  
 RT mediates reproductive and circadian responses."  
 RL Neuron 13:1177-1185(1994).  
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. LIKELY TO MEDIATES  
 CC THE PERCEPTIVE AND CIRCADIAN ACTIONS OF MELATONIN. THE ACTIVITY  
 CC OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G  
 CC PROTEINS THAT INHIBITS ADENYLYLATE CYCLASE ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: AT LEAST IN THE BRAIN, MORE PRECISELY IN THE  
 CC PARS TENUERIS AND THE SUPRACHIASMATIC NUCLEUS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb.slb.ch/announce/>  
 CC or send an email to [license@isb.slb.ch](mailto:license@isb.slb.ch)).  
 CC  
 CC EMBL: U14409; AA57191.1;  
 CC INTERPRO: IPR000276;  
 CC PFM: PFO0001; 7tm\_1; 1.  
 CC PROSITE: PS00237; G-PROTEIN\_RECEP\_FL\_1; PARTIAL.  
 CC PROSITE: PS0262; G-PROTEIN\_RECEP\_FL\_2; 1.  
 CC G-protein coupled receptor. Transmembrane. Glycoprotein.  
 CC  
 CC NON-TER 1  
 CC TRANSSEM 19 35 1 (POTENTIAL).  
 CC TRANSSEM 62 82 2 (POTENTIAL).  
 CC TRANSSEM 115 135 3 (POTENTIAL).  
 CC NON-TER 156  
 CC SEQUENCE 156 AA: 18214 MW: 2B5SEVAQFEG6RARI CRG64;  
 47.4% Score 717.5; DB 1; Length 156;  
 Best Local Similarity 84.6%; Pred. No. 3,2e-43;  
 Matches 132: Conservative 12; Mismatches 11; Indels 1; Gaps 1;  
 66 CYICHSLKCDKLYSSKNSLCVLLIMLTL-AAVPLNLRGSLQYPRYSCTFAQSSA 124  
 DB 1 CYICHSLKDRIVSNKNSLCVFLIMLTLIAIKENLDTGLVPPRYSCFQSSA 60  
 QY 125 YTTAVVVFHFLVPMITIVFCYLRITWILVLOVPQVKKPDKRKLPHDFRNV 184  
 DB 61 YTTAVVVFHFLVPMITIVFCYLRITWILVLOVPQVKKPDKRKLPHDFRNV 120  
 QY 185 FAICWAPLNFIGLVAASDPASVPRIPMLFVASIY 220  
 DB 121 FALCWAPLNFIGLVAASDPASVPRIPMLFVASIY 156

```

RESULT 14
MLX_MOUSE STANDARD: PRT: 583 AA
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
MELANONIN-RELATED RECEPTOR (H9).
GPR50.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
SEQUENCE FROM N.A.
MEDLINE-99134305; PubMed-9933574;
Gubitz A.K., Peppert S.M.;
Assignment of the melatonin-related receptor to human chromosome X
(GPR50) and mouse chromosome X (GPR50).
Genomics 55:248-251(1999).
- FUNCTION: DOES NOT BIND MELANONIN.
- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
EMBL: AF065145; AAC21462.1; ALT_INIT.
MGD: MGI:133877; GPR50.
INTERPRO: IPR000276; -.
IPRfam: IPR000011; 7tm_1.1.
PRINTS: PR01151; MELANONINXR.
PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
PROSITE: PS00262; G_PROTEIN_RECPT_FL_2; 1.
G-protein coupled receptor; Transmembrane.
DOMAIN 1 30
TRANSMEM 31 51
DOMAIN 52 64
TRANSMEM 65 85
DOMAIN 86 103
TRANSMEM 104 123
DOMAIN 125 143
TRANSMEM 144 164
DOMAIN 165 188
TRANSMEM 189 209
DOMAIN 210 239
TRANSMEM 240 260
DOMAIN 261 273
TRANSMEM 274 294
DOMAIN 295 583
DISULFID 101 178
SEQUENCE 583 AA: 64306 MW: 6713570.434 kDa 2426 Cys64.

Query Match 47.2% Score 714.5; DB 1; Length 583;
Best Local Similarity 48.4%; Pred. No. 1.5e-42;
Matches 134; Conservative 59; Mismatches 79; Indels 5; Gaps 3;
1 GATPVSATLAAVLAIVPYPLVLSIFNNQNLGLHGVSGFLMGSLVGSIFNIGI 60
|||||
63 GNIPVASLSVALDLVAIVPYPLVLSIFNNQNLGLHGVSGFLMGSLVGSIFNIGI 122
|||||
61 AINRYCYICHSCDKCLYSKNSLCLVLLIMLTLA-AVLPNLRGTLQYEPRIYSCFPAQ 119
|||||
123 AINRYCYICHSLQYKRIFSLRNTGILYLVATWYLVAVLPNRYIOTIEYDRPTIYCI 192
|||||

```

```

Query Match 44.1% Score 667.5; DB 1; Length 154;
Best Local Similarity 81.8%; Pred. No. 8.6e-40;
Matches 126; Conservative 12; Mismatches 15; Indels 1; Gaps 1;
120 SVSSATIAVVFHFLVPMIVFCTPLIMLVLPVQVQKPRPKLPHDPNFVTF 179
|||
183 VNNPAPFVITVCHFLVPLIVGYCYTKIMIKVLARD--PAQNDQNFVAPVNFITF 240
|||
180 VVFLPFAICAPINFLGLAVASDASMPRIPEMELVASYAYANFSCINATISGWON 239
|||||
241 VITLFAVCEPYNVLTVAIVPEKEMASKIPMNTIAVAGIAFNSCINATITVGIN 300
|||||
240 FKEEYRIVSLVAVFVDSNDVADRVKWPSP 276
|||||
301 FKEEYWTIFHAMPPIFLSHLSDI--RETWETRAL 335
|||||

RESULT 15
MLA_PIG STANDARD: PRT: 154 AA.
ID MLA_PIG
AC 002781;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DT MELANONIN RECEPTOR TYPE 1A (MEL-1A-R) (FRAGMENT).
GN MNRIA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
[1]
SEQUENCE FROM N.A.
TISSUE-HYPOTHALAMUS, AND PITUITARY;
MEDLINE-97262109; PubMed-9107687;
Messier L.A., Wang L., Torggler C.K., Yezle M., Chardon P., Pomp D.,
Kowacki J.E., Rands W., Crawford A.M., Notter D.R.,
Rothschild M.F.;
Mapping of the melatonin receptor 1a (MNRIA) gene in pigs, sheep,
rat and cattle.
Mamm Genome 8:368-370(1997).
- FUNCTION: HIGH AFFINITY RECEPTOR FOR MELANONIN LIKELY TO MEDIATES
THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELANONIN. THE ACTIVITY
OF THIS RECEPTOR IS MEDIATED BY PERISSIT TOXIN SENSITIVE G
PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
EMBL: U73326; AAC48726.1; -.
INTERPRO: IPR000276; -.
IPRfam: IPR000011; 7tm_1.1.
PRINTS: PS00237; G_PROTEIN_RECPT_FL_1; 1.
PROSITE: PS00262; G_PROTEIN_RECPT_FL_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 1 1
TRANSMEM 2 19
DOMAIN 20 40
TRANSMEM 41 62
DOMAIN 63 83
TRANSMEM 84 115
DOMAIN 116 136
TRANSMEM 137 149
DOMAIN 150 154
SEQUENCE 154 AA: 179600 MW: 19585442.785 kDa 93 Cys64.

```

Tue Feb 20 11:43:06 2001

us-09-226-046-6.rsp

Page 11

23 65 YCNIGCSLCKCKLYSSKNSLCYVLLTLLTLL--AAVLPNPNRPLGTYFPEDYASCTFAQSVSS 123  
 24 1 YCNIGCSLCKCKLYSSKNSLCYVLLTLLTLL--AAVLPNPNRPLGTYFPEDYASCTFAQSVSS 123  
 25 1 YCNIGCSLCKCKLYSSKNSLCYVLLTLLTLL--AAVLPNPNRPLGTYFPEDYASCTFAQSVSS 60  
 26 124 AYTAAVYVHFVLPVMIYIEGCIPLMITIVILQVPPKPPDKPKLPHDFRNFVMTFVVEV 183  
 27 124 AYTAAVYVHFVLPVMIYIEGCIPLMITIVILQVPPKPPDKPKLPHDFRNFVMTFVVEV 183  
 28 61 AYTAAVYVHFVLPVMIYIEGCIPLMITIVILQVPPKPPDKPKLPHDFRNFVMTFVVEV 120  
 29 184 LFAICMAPLNFILGLAVASDPASWVPRIPIEWLEVA 217  
 30 121 LFAICMAPLNFILGLAVASDPASWVPRIPIEWLEVA 154

Search completed. February 19, 2001, 14:36:38  
Job time: 3255 sec





```

78 GVVFVSLAVADLVAVPPLVPLALASIVNNGKSLSLHQLSLGFLMGLSVIGSVPTIGI 137
61 AINRYVICHSLKCKLYSKNSKSLCYVLLIMLT-AAVPLNRLRGTIOYEPRIYSCFQA 119
148 AINRYVICHSLKCKLYSKNSKSLCYVLLIMLTAAVPLNRLRGTIOYEPRIYSCFQA 197
129 VSVAVTIAVAVVHFLVLMIVIFVYFLVILVLCVPEVKKIKPKIKHGFNFVTF 179
198 VSVAVTIAVAVVHFLVLMIVIFVYFLVILVLCVPEVKKIKPKIKHGFNFVTF 257
140 VVVFVFAICMAPLNFICGLAVASDPASMPRIPEMLFVASVYMAVFNCLNAIISGVNQN 239
268 VVVFVFAICMAPLNFICGLAVASDPASMPRIPEMLFVASVYMAVFNCLNAIISGVNQN 317
240 FPKFVPIVSVTAVPVEFVSSNDVADPVKPKSPCLMTNNNVKVSU 298
418 FPKFVPIVSVTAVPVEFVSSNDVADPVKPKSPCLMTNNNVKVSU 366

RESULT 2
Q92289 PRELIMINARY PRT 325 AA.
01-MAY-1999 (TREMblrel. 10, created)
01-MAY-1999 (TREMblrel. 10, last sequence update)
01-OCT-2000 (TREMblrel. 15, last annotation update)
MELATONIN RECEPTOR MELLN (FRAGMENT).
MuscleTectus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetidae;
Musotricus.
NCBI_TaxID=10036.
11
SEQUENCE FROM N.A.
TISOR-SUPRACHIASMATIC NUCLEI.
Gautier F., Schuster G., Poltel V.-J., Peyet P., Masson-Peyet M.:
"Altering experimental and developmental expression of both melatonin
receptor Mella mRNAs and melatonin binding sites in the Syrian hamster
suprachiasmatic nuclei".
Brain Res. Mol. Brain Res. 90:1-9(1998).
EMBL AF061158 AAC67241.1.
INTERPRO: IPR000276.
INTERPRO: IPR000611.
IPR002781.
IPR000001: 7tm1.1.
PRINTS: PR00237. GPCRPHODPSN.
PRINTS: PR00857. MELATONINR.
PRINTS: PR01012. NRPEPTIDYR.
PRINTS: PR01149. MELATONINLAR.
PROSITE: PS00237. G_PROTEIN_RECEPTOR. UNKNOWN_1.
RECEPTOR.
N-TER 1 1
N-TER 425 425
SEQUENCE 325 AA: AAG4CBG97BCAGAS CPG64.

Query Match 81.5% Score 1234.5; DB 11; Length 325;
Best Local Similarity 86.2%; Pred. No. 4, be-97;
Matches 242; Conservative 18; Mismatches 18; Indels 1; Gaps 1;

```

```

QY 180 VVVFVFAICMAPLNFICGLAVASDPASMPRIPEMLFVASVYMAVFNCLNAIISGVNQN 239
DB 237 VVVFVFAICMAPLNFICGLAVASDPASMPRIPEMLFVASVYMAVFNCLNAIISGVNQN 296
QY 240 FPKFVPIVSVTAVPVEFVSSNDVADPVKPKSPCLMTNNNVKVSU 298
DB 240 FPKFVPIVSVTAVPVEFVSSNDVADPVKPKSPCLMTNNNVKVSU 325

RESULT 3
Q92290 PRELIMINARY PRT 383 AA.
ID Q92290
AC Q92290
DT 01-MAY-2000 (TREMblrel. 13, created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DT 01-OCT-2000 (TREMblrel. 15, last annotation update)
DE MELATONIN RECEPTOR MELLN.
OS Ocorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei;
OC Actinopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC troctactinopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
CX NCBI_TaxID=8022.
RN 11
SEQUENCE FROM N.A.
RP Mazurais D., Brierley I., Kah O., Williams L.:
"Expression of rainbow trout melatonin receptor".
Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
EMBL AF156262 AAF00191.1.
INTERPRO: IPR000025.
INTERPRO: IPR000276.
INTERPRO: IPR000611.
INTERPRO: IPR002016.
INTERPRO: IPR002278.
IPR000001: 7tm1.1.
IPR00237. GPCRPHODPSN.
PRINTS: PR00237. GPCRPHODPSN.
PRINTS: PR00857. MELATONINR.
PRINTS: PR01012. NRPEPTIDYR.
PRINTS: PR01149. MELATONINLAR.
PROSITE: PS00237. G_PROTEIN_RECEPTOR. UNKNOWN_1.
PROSITE: PS00456. FPKXITASE_2. UNKNOWN_1.
RECEPTOR.
N-TER 1 1
N-TER 383 AA: 1PFAEB61127E570 CPG64.

Query Match 80.0% Score 1211.5; DB 13; Length 383;
Best Local Similarity 77.9%; Pred. No. 4, be-95;
Matches 225; Conservative 32; Mismatches 31; Indels 1; Gaps 1;

```



01-MAY-1997 (TREMELrel. 03, Created)  
 01-MAY-1997 (TREMELrel. 03, Last sequence update)  
 01-OCT-2000 (TREMELrel. 15, Last annotation update)  
 MEL-1C(A) MELATONIN RECEPTOR  
 Xenopus laevis (African clawed frog)  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Amphibia: Batrachia: Anura: Mesobatrachia: Pipridae: Pipidae:  
 Xenopodinae: Xenopus.  
 NCBI\_TaxID=8355;  
 (1)  
 SEQUENCE FROM N.A.  
 TISSUE=SKIN;  
 Jockers R., Petit L., Lacroix I., de Coppet P., Barrett P.,  
 Moran J.P., Guardiola B., Delagrègne P., Marullo S., Strosberg A.D.,  
 Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 EMBL: U67882; AAB48392.1;  
 EMBL: U67879; AAB48391.1;  
 INTERPRO: IPR000025;  
 INTERPRO: IPR000025;  
 INTERPRO: IPR000025;  
 INTERPRO: IPR000025;  
 PIRAM: PF00001; 7tm\_1; 1;  
 PRINTS: PR00857; MELATONINR  
 PRINTS: PR01150; MELATONINR  
 PRINTS: PR00237; G-PROTEIN RECEPTOR; UNKNOWN\_1;  
 PROSITE: PS00237; G-PROTEIN RECEPTOR; UNKNOWN\_1;  
 SEQUENCE 354 AA; 39931 MW; DCF78D208F0C97A6 CRC64;

Query Match 70.0%; Score 1059.5; DB 13; Length 354;  
 Best Local Similarity 67.4%; Pred. No. 3,3e-82;  
 Matches 189; Conservative 49; Mismatches 42; Indels 1; Gaps 1;

01-MAY-1997 (TREMELrel. 03, Created)  
 01-MAY-1997 (TREMELrel. 03, Last sequence update)  
 01-OCT-2000 (TREMELrel. 15, Last annotation update)  
 MEL-1C(B) MELATONIN RECEPTOR  
 Xenopus laevis (African clawed frog)  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Amphibia: Batrachia: Anura: Mesobatrachia: Pipridae: Pipidae:  
 Xenopodinae: Xenopus.  
 NCBI\_TaxID=8355;  
 (1)  
 SEQUENCE FROM N.A.  
 TISSUE=SKIN;  
 Jockers R., Petit L., Lacroix I., de Coppet P., Barrett P.,  
 Moran J.P., Guardiola B., Delagrègne P., Marullo S., Strosberg A.D.,  
 Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 EMBL: U67882; AAB48392.1;  
 EMBL: U67881; AAB48391.1;  
 01-MAY-1997 (TREMELrel. 03, Created)  
 01-MAY-1997 (TREMELrel. 03, Last sequence update)  
 01-OCT-2000 (TREMELrel. 15, Last annotation update)  
 MEL-1C(B) MELATONIN RECEPTOR  
 Xenopus laevis (African clawed frog)  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Amphibia: Batrachia: Anura: Mesobatrachia: Pipridae: Pipidae:  
 Xenopodinae: Xenopus.  
 NCBI\_TaxID=8355;  
 (1)  
 SEQUENCE FROM N.A.  
 TISSUE=SKIN;  
 Jockers R., Petit L., Lacroix I., de Coppet P., Barrett P.,  
 Moran J.P., Guardiola B., Delagrègne P., Marullo S., Strosberg A.D.,  
 Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 EMBL: U67882; AAB48392.1;  
 EMBL: U67881; AAB48391.1;

INTERPRO: IPR000025;  
 INTERPRO: IPR000025;  
 INTERPRO: IPR000025;  
 INTERPRO: IPR000025;  
 PIRAM: PF00001; 7tm\_1; 1;  
 PRINTS: PR00857; MELATONINR  
 PRINTS: PR01150; MELATONINR  
 PRINTS: PR00237; G-PROTEIN RECEPTOR; UNKNOWN\_1;  
 PROSITE: PS00237; G-PROTEIN RECEPTOR; UNKNOWN\_1;  
 SEQUENCE 354 AA; 39931 MW; FDE6C2E8E335561D CRC64;

Query Match 69.3%; Score 1049.5; DB 13; Length 354;  
 Best Local Similarity 67.0%; Pred. No. 2.4e-81;  
 Matches 189; Conservative 49; Mismatches 43; Indels 1; Gaps 1;

01-MAY-1997 (TREMELrel. 03, Created)  
 01-MAY-1997 (TREMELrel. 03, Last sequence update)  
 01-OCT-2000 (TREMELrel. 15, Last annotation update)  
 MEL-1C(A) MELATONIN RECEPTOR  
 Xenopus laevis (African clawed frog)  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Amphibia: Batrachia: Anura: Mesobatrachia: Pipridae: Pipidae:  
 Xenopodinae: Xenopus.  
 NCBI\_TaxID=8355;  
 (1)  
 SEQUENCE FROM N.A.  
 TISSUE=SKIN;  
 Jockers R., Petit L., Lacroix I., de Coppet P., Barrett P.,  
 Moran J.P., Guardiola B., Delagrègne P., Marullo S., Strosberg A.D.,  
 Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 EMBL: U67882; AAB48392.1;  
 EMBL: U67881; AAB48391.1;  
 01-MAY-1997 (TREMELrel. 03, Created)  
 01-MAY-1997 (TREMELrel. 03, Last sequence update)  
 01-OCT-2000 (TREMELrel. 15, Last annotation update)  
 MEL-1C(B) MELATONIN RECEPTOR  
 Xenopus laevis (African clawed frog)  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Amphibia: Batrachia: Anura: Mesobatrachia: Pipridae: Pipidae:  
 Xenopodinae: Xenopus.  
 NCBI\_TaxID=8355;  
 (1)  
 SEQUENCE FROM N.A.  
 TISSUE=SKIN;  
 Jockers R., Petit L., Lacroix I., de Coppet P., Barrett P.,  
 Moran J.P., Guardiola B., Delagrègne P., Marullo S., Strosberg A.D.,  
 Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 EMBL: U67882; AAB48392.1;  
 EMBL: U67881; AAB48391.1;

01-MAY-1997 (TREMELrel. 03, Created)  
 01-MAY-1997 (TREMELrel. 03, Last sequence update)  
 01-OCT-2000 (TREMELrel. 15, Last annotation update)  
 MEL-1C(A) MELATONIN RECEPTOR  
 Xenopus laevis (African clawed frog)  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Amphibia: Batrachia: Anura: Mesobatrachia: Pipridae: Pipidae:  
 Xenopodinae: Xenopus.  
 NCBI\_TaxID=8355;  
 (1)  
 SEQUENCE FROM N.A.  
 TISSUE=SKIN;  
 Jockers R., Petit L., Lacroix I., de Coppet P., Barrett P.,  
 Moran J.P., Guardiola B., Delagrègne P., Marullo S., Strosberg A.D.,  
 Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 EMBL: U67882; AAB48392.1;  
 EMBL: U67881; AAB48391.1;  
 01-MAY-1997 (TREMELrel. 03, Created)  
 01-MAY-1997 (TREMELrel. 03, Last sequence update)  
 01-OCT-2000 (TREMELrel. 15, Last annotation update)  
 MEL-1C(B) MELATONIN RECEPTOR  
 Xenopus laevis (African clawed frog)  
 Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Amphibia: Batrachia: Anura: Mesobatrachia: Pipridae: Pipidae:  
 Xenopodinae: Xenopus.  
 NCBI\_TaxID=8355;  
 (1)  
 SEQUENCE FROM N.A.  
 TISSUE=SKIN;  
 Jockers R., Petit L., Lacroix I., de Coppet P., Barrett P.,  
 Moran J.P., Guardiola B., Delagrègne P., Marullo S., Strosberg A.D.,  
 Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
 EMBL: U67882; AAB48392.1;  
 EMBL: U67881; AAB48391.1;

Query Match 42.5%; Score 643.5; DB 13; Length 162;  
 Best Local Similarity 71.0%; Pred. No. 2.6e-47;  
 Matches 115; Conservative 25; Mismatches 21; Indels 1; Gaps 1;







DB 391 DS 392

```

>RESULT 15
>Q9NKG26 PRELIMINARY: PRI: 392 AA
>01-OCT-2000 (TREMBLrel. 15, Created)
>01-OCT-2000 (TREMBLrel. 15, Last sequence update)
>01-OCT-2000 (TREMBLrel. 15, Last annotation update)
>TREHALOSE RECEPTOR 1.
>TREHALOSE RECEPTOR 1.
>Drosophila melanogaster (Fruit fly).
>Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
>Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
>Ephydroidea; Drosophilidae; Drosophila.
>NCBI_TaxID=7227;
>[1]
>SEQUENCE FROM N.A.
>Ishimoto H.;
>"Molecular and genetic identification of a taste receptor gene for
>trehalose in Drosophila."
>Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
>EMBL: AB034204; FAA95353.1;
>Receptor.
>SEQUENCE 392 AA: 43827 MW: 16671055D40D9E8 CRC64:

```

```

Query Match 17.48; Score 263, DB 5; Length 392;
Best Local Similarity 25.48; Pred. No. 1, 1e-14;
Matches 72; Conservative 53; Mismatches 107; Indels 52; Gaps 9;

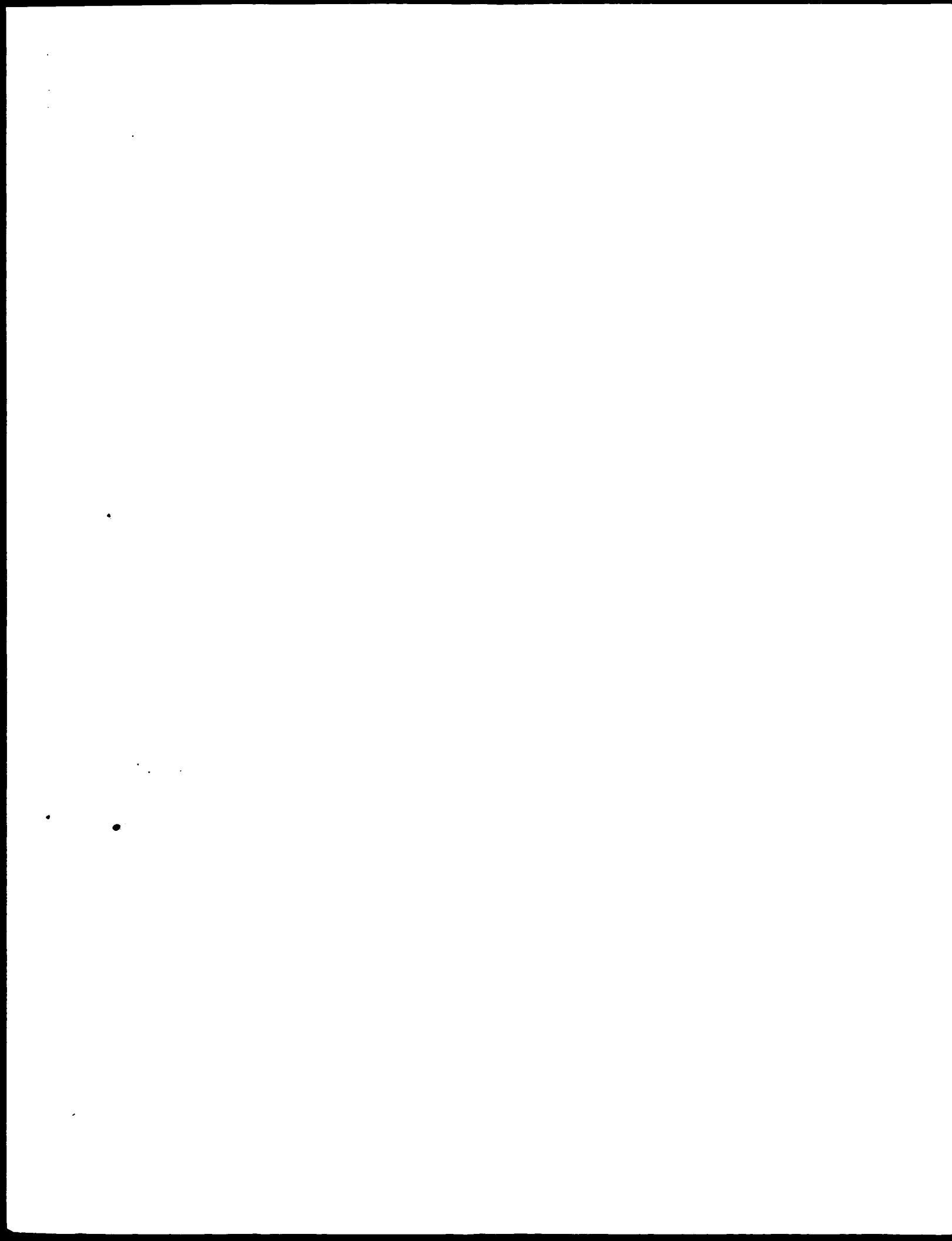
```

```

>4 FVVSIAVADLVVAIYPIYPLVMSIFNNGMNLGYLHCQVSGFLMGLSVTGSIFNITGIAIN 63
>74 FVVISLISDLDFCSFSLPLAVRPFQESWTFGLCKIFFVIFYGNVAVSLSMWGITLN 133
>64 PYCPT-CHSLKGVLYSGFNSGVVLLIMLT-AAVLPNLR--GTLQYEPRIYSGTFQ 119
>134 RYLIACHS-RYSQIVKPKFTLQLFVMAVSELLPLILGIWEMGDEATFSCITLK 192
>120 SVSAGVIAVVFVFLVPMIIVIFCYLIMLVLVQVQRYKPDPRKPKPHDFRNF--- 175
>193 KEGRSIRKTLFVIGFLPLCLVIIVSYSCIYIV-----PHQKKIRNHD--NFOIA 242
>176 -----VTMFVVFVLFALCMAPLNFIGLAVASDPASMY 207
>243 AKGSSSSGGSGSYMTTCTRKAREDNRLVVMVTLFCLVCLPL-MLANVDDERNIST 301
>268 FRIPFWLFAVYVAVYFNSCLNATISGVNQNFRKFRRIIVSL 251
>302 P-----WLIHIVAVMAWSSVINPIIYAASNPNRYVAYKTFALL 341

```

Search completed: February 18, 2001, 16:46:32  
 Job time: 8250 sec



(without alignments)  
1498.522 Million cell updates/sec

Scoring table:	IDENTITY_NUC	Gapext
	10 0	1 0

Searched: 1118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing:	Minimum Match	0%
	Maximum Match	100%

Listing first 45 summaries

Database

```

1: qb ba1.*
2: qb ba2.*
3: qb_om.*
4: qb_ox.*
5: qb-pl1.*
6: qb-pl1.*
7: qb-pl2.*
8: qb-pl1.*
9: qb-pl2.*
10: qb-pl3.*
11: qb_ox.*
12: qb_sy.*
13: qb_un.*
14: em_fun.*
15: em_hum1.*
16: em_hum2.*
17: em_in.*
18: em_om.*
19: em_ox.*
20: em_ov.*
21: em_pat.*
22: em_pl.*
23: em_pl.*
24: em_pl.*
25: em_rls.*
26: em_sy.*
27: em_un.*
28: em_v.*
29: qb_ox.*
30: qb-pl1.*
31: qb-pl2.*
32: qb-pl3.*
33: qb-pl3.*
34: qb-pl4.*
35: em_ba1.*
36: em_ba2.*
37: em_ba3.*
38: em_ha1.*
39: em_ha2.*
40: em_ha3.*
41: em_ha5.*
42: em_ha6.*
43: em_ha7.*

```

44:	em	htg9:	*
45:	em	htg9:	*
46:	em	htglu:	*
47:	em	huma:	*
48:	em	huma:	*
49:	em	huma:	*
50:	em	huma:	*
51:	qb	pr5:	*
52:	qb	pr6:	*
53:	qb	pr7:	*
54:	qb	htgl:	*
55:	qb	htg2:	*
56:	qb	htg3:	*
57:	qb	htg4:	*
58:	qb	htg5:	*
59:	qb	htg6:	*
60:	qb	htg7:	*
61:	qb	htg8:	*
62:	qb	htg9:	*
63:	qb	htgl:	*
64:	qb	htgl:	*
65:	qb	htgl:	*
66:	qb	htgl:	*
67:	qb	htgl:	*
68:	qb	htgl:	*
69:	qb	htgl:	*
70:	qb	htgl:	*
71:	qb	htgl:	*
72:	qb	htgl:	*
73:	qb	htgl:	*
74:	qb	htgl:	*
75:	qb	htgl:	*
76:	qb	htgl:	*
77:	qb	htgl:	*
78:	qb	htgl:	*
79:	qb	htgl:	*
80:	qb	htgl:	*
81:	qb	htgl:	*
82:	qb	htgl:	*
83:	qb	htgl:	*
84:	qb	htgl:	*
85:	qb	htgl:	*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result	Score	Query	Match	Length	DB	ID	Description
1	1085	100.0	1085	53	HSU14108	U14108 Human Mel-1	
2	1085	100.0	1085	81	AR026631	AR026631 Sequence	
3	1040.4	95.9	1050	81	E12845	E12845 cDNA oncodi	
4	83.4	80.2	1250	9	AP024433	AP024433 Homo sapi	
5	870.4	80.2	149317	58	AC015601	AC015601 Homo sapi	
6	83.6	75.9	867	81	AC026630	AC026630 Sequence	
7	764	70.4	1149	3	CA014103	CA014103 Ovis arie	
8	764	70.4	1149	81	AR026632	AR026632 Sequence	
9	756	69.7	1219	3	AP045219	AP045219 Ovis arie	
10	746	68.8	1362	11	XM055110	XM055110 Ovis arie	
11	746	67.8	1593	11	XM055222	XM055222 Mus musculu	
12	717	65.1	1057	5	AF026632	AF026632 Sequence	
13	683.4	63.0	977	11	AF061158	AF061158 Mesocricet	
14	679.8	52.7	982	11	AF136341	AF136341 Rattus no	
15	679.8	52.7	982	57	AF015259	AF015259 Homo sapi	
16	615.4	56.7	1065	4	GC031820	GC031820 Gallus gall	
17	583.8	53.8	771	3	BT079327	BT079327 Bos tauru	
18	579.2	53.4	1152	4	AF156262	AF156262 Oncorhyn	
19	459.2	46.0	1266	4	GC011821	GC011821 Gallus gall	
20	497	45.8	1104	4	AF188871	AF188871 Esox lucii	
21	483.8	44.6	1105	53	HS025341	HS025341 Human Melib	

22 481.8 44.5 1105 81 A075533 Sequence  
23 473.8 41.7 1141 4 X1067881  
24 473.8 41.7 1141 4 X1067881  
25 473.8 41.7 1141 4 X1067881  
26 472.2 43.5 1147 81 A597542  
27 472.2 43.5 1147 81 A597542  
28 472.2 43.5 1147 81 A597542  
29 472.2 43.5 1147 81 A597542  
30 472.2 43.5 1147 81 A597542  
31 472.2 43.5 1147 81 A597542  
32 472.2 43.5 1147 81 A597542  
33 472.2 43.5 1147 81 A597542  
34 472.2 43.5 1147 81 A597542  
35 472.2 43.5 1147 81 A597542  
36 472.2 43.5 1147 81 A597542  
37 472.2 43.5 1147 81 A597542  
38 472.2 43.5 1147 81 A597542  
39 472.2 43.5 1147 81 A597542  
40 472.2 43.5 1147 81 A597542  
41 472.2 43.5 1147 81 A597542  
42 472.2 43.5 1147 81 A597542  
43 472.2 43.5 1147 81 A597542  
44 472.2 43.5 1147 81 A597542  
45 472.2 43.5 1147 81 A597542

## ALIGNMENTS

RESULT 1  
HSD14108 1085 bp mRNA PRI 01-NOV-1996  
DEFINITION Human Mel-1a melatonin receptor mRNA, complete cds  
ACCESSION U14108  
VERSION 014108.1 01-NOV-1996  
KEYWORDS  
SOURCE human  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Eumetazoa; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 1085)  
AUTHORS Reppert, S.M., Weaver, D.R. and Ebisawa, T.  
TITLE Cloning and characterization of a mammalian melatonin receptor that  
mediates reproductive and circadian responses  
JOURNAL NEURON 13 (1): 1127-1135 (1994)  
MEDLINE 95033231  
PMID 75033231

REFERENCE 2 (bases 1 to 1085)  
AUTHORS Reppert, S.M.  
TITLE Direct Submission  
JOURNAL Submitted (29-NOV-1994) Steven M. Reppert, Chronobiology,  
Children's Services, Massachusetts General Hospital, 22 Fruit St.,  
Boston, MA 02114, USA  
LOCATION/CONTAINER 1, 1085

## FEATURES

5' UTR

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

/db\_xref="taxon:9606"

BASE COUNT  
226 A 224 C 279 G 257 T

Query Match 100.0% Score 1085.00 Length 1085  
Pos Local Similarity 100.0% Pos Local Similarity 100.0%  
Matches 1085 Conservative 0 Memory 0 Gaps 0  
1 481.8 44.5 1105 81 A075533 Sequence  
2 473.8 41.7 1141 4 X1067881  
3 473.8 41.7 1141 4 X1067881  
4 473.8 41.7 1141 4 X1067881  
5 472.2 43.5 1147 81 A597542  
6 472.2 43.5 1147 81 A597542  
7 472.2 43.5 1147 81 A597542  
8 472.2 43.5 1147 81 A597542  
9 472.2 43.5 1147 81 A597542  
10 472.2 43.5 1147 81 A597542  
11 472.2 43.5 1147 81 A597542  
12 472.2 43.5 1147 81 A597542  
13 472.2 43.5 1147 81 A597542  
14 472.2 43.5 1147 81 A597542  
15 472.2 43.5 1147 81 A597542  
16 472.2 43.5 1147 81 A597542  
17 472.2 43.5 1147 81 A597542  
18 472.2 43.5 1147 81 A597542  
19 472.2 43.5 1147 81 A597542  
20 472.2 43.5 1147 81 A597542  
21 472.2 43.5 1147 81 A597542  
22 472.2 43.5 1147 81 A597542  
23 472.2 43.5 1147 81 A597542  
24 472.2 43.5 1147 81 A597542  
25 472.2 43.5 1147 81 A597542  
26 472.2 43.5 1147 81 A597542  
27 472.2 43.5 1147 81 A597542  
28 472.2 43.5 1147 81 A597542  
29 472.2 43.5 1147 81 A597542  
30 472.2 43.5 1147 81 A597542  
31 472.2 43.5 1147 81 A597542  
32 472.2 43.5 1147 81 A597542  
33 472.2 43.5 1147 81 A597542  
34 472.2 43.5 1147 81 A597542  
35 472.2 43.5 1147 81 A597542  
36 472.2 43.5 1147 81 A597542  
37 472.2 43.5 1147 81 A597542  
38 472.2 43.5 1147 81 A597542  
39 472.2 43.5 1147 81 A597542  
40 472.2 43.5 1147 81 A597542  
41 472.2 43.5 1147 81 A597542  
42 472.2 43.5 1147 81 A597542  
43 472.2 43.5 1147 81 A597542  
44 472.2 43.5 1147 81 A597542  
45 472.2 43.5 1147 81 A597542











[illegible]



D8	806	TGTCACCATATGTTTGGAGTTTCTTGCCGCTGTTCGCATTGTCGAGCGCTCCTCGTAGACTTCA	865
OY	802	ttgacctggccgtgcctcctgaaccccccaagatgatgccttagatcccagaagtgcctt	861
DB	866	TTTTGTTTCTGTTTGTGTTTGGTAAGTAAAGGATAATGAGATATGCAATGCAATGCGAGTGGT	925
OY	862	ttagcgcaacttaactaaatggcgattttaaacagctgttcctcaatgccatatatacaggac	921
LE	926	TTTGTCGTCTAGTTATATATAGGTCATATTTAAGAAGTGTGTTTGAATGCGATCATATATGAC	985
OY	922	tactaacccaattctcaggaaggaatatacaggaagaattatagctgcctcttatagaaca	981
DB	986	TACTCAACCAAAATTTCCAGCCAGCATATACAAGAAAATTTACTGCTGATGTTTACCACCA	1045
OY	982	gagttctcttgtagaacactctaagacgtgcgcgataagggttaaaggaaccgtcttc	1041
DB	1046	AATGTTCTTTTGTGTAAGTTTCTTAATCATATGATGAPATATGAAATTAAACGCCAACCTGTTT	1105
OY	1042	cactatgacccacaataatgatgataaagtatgacctgccttcaa	1085
DB	1106	CATTATAGCCACCACTATACCTATATAGGTGACCTGCTTTAA	1149
RESULT	9		
LOCUS	AF045219	1219 bp	MRNA MAM 11-FEB-1998
DEFINITION	Ovis aries Mel ja melatonin receptor mRNA complete cds.		
ACCESSION	AF045219		
VERSION	AF045219.1 GI:2865610		
KEYWORDS			
SOURCE	Sheep.		
ORGANISM	Ovis aries		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Artiodactyla; Cetartiodactyla; Fuminantia; Bovora; Ruminantia; Bovidae; Caprinae; Ovis. 1 (bases 1 to 1219) Barrett,P., Conway,S., Jockers,R., Strosberg,A.D., Guadalupe-Lemaitre,B., Delagrènge,P. and Morgan,P.J. Cloning and functional analysis of a polymorphic variant of the ovine Mel ja melatonin receptor Biochim Biophys Acta 1356 (3) : 299-307 (1997)		
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
Source			
CDs			
BASE COUNT	251 a 337 c 330 g 301 t		
ORIGIN			

```
Query Match          69.78; Score 756; DB 3; Length 1219;  
Best Local Similarity 92.7%; Prod. No. 90-128  
Matches 880, Conservative 0; Mismatches 175; Indels 9; Gaps 1
```

[illegible]

DE 1091 CATMAIACNANCSJAMACTAGAAAACCTGCGGTAA 1124

RESULT 10











REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

1 (bases 1 to 304430)  
Hirose, H., Linton, L., Nishbaum, C. and Lander, E.  
Homo sapiens chromosome 4, clone RP11-390N2  
Unpublished  
2 (bases 1 to 304430)

Burton, R., Linton, L., Nishbaum, C., Lander, E., Allen, N., Anderson, M.,  
Kaldwin, J., Patra, N., Postel, P., Ruzsaski, J., Bokkhalter, E.,  
Brown, A., Castle, A., Collins, M., Collins, S., Collymore, A.,  
Coker, D., Corbellino, K., Dekar, K., Domingo, M., Fong, J., Foy, M.,  
Garcia, J., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,  
Hollander, J., Jandova, S., Grant, C., Haros, R., Heaford, A., Horton, L.,  
Howard, J., Johnson, R., Jones, C., Kann, L., Karasik, A., Klein, J.,  
Lander, E., Linton, L., Linton, L., MacDonald, P., Maritz, N.,  
McKean, P., McQuinn, A., McKinnon, K., McLaughlin, T., Melnick, J.,  
Mortrud, J., Nayak, J., Norman, C., H., O'Connor, T., O'Connell, P.,  
Petersen, K., Pitts, V., Pilon, P., Poy, A., Sadava, P., Searcy, J.,  
Shapiro, J., Shih, N., Stojanovic, N., Sutherland, A., Talamas, J.,  
Toshiba, S., Turrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,  
Wymant, C., Ye, W., Zimmer, A. and Zody, M.

Submitted (21-Oct-1999) Whitehead Institute/MIT Center for Genome  
Research, 420 Charles Street, Cambridge, MA 02141, USA  
On Jul 13, 2000 this sequence version replaced at 553385.  
All repeats were identified using RepeatMasker.  
Smith, A.F.A. & Green, P. (1996:1997)  
http://www.washington.edu/gen/RepeatMasker.html

Genome Center  
Center: Whitehead Institute/MIT Center for Genome Research  
Center code: W1B8  
Web site: <http://www.sas.wi.mit.edu>  
Contract: sequenced-submissions@genome.wi.mit.edu  
Project information  
Center project name: L1754  
Center clone name: 390\_N2

\* NOTE: This record contains 323 individual  
\* sequenced reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

778 877: gap of 100 bp  
878 1694: contig of 822 bp in length  
1700 1799: gap of 100 bp  
1800 2604: contig of 805 bp in length  
2605 2734: gap of 100 bp  
2705 3480: contig of 776 bp in length  
3481 4580: gap of 100 bp  
4581 4384: contig of 804 bp in length  
4385 4444: gap of 100 bp  
4485 5295: contig of 811 bp in length  
5296 5395: gap of 100 bp  
5396 5199: contig of 804 bp in length  
6200 6239: gap of 100 bp  
6200 7080: contig of 781 bp in length  
7081 7180: gap of 100 bp  
7181 7947: contig of 817 bp in length  
7948 8047: gap of 100 bp  
8048 8904: contig of 807 bp in length  
8905 9094: gap of 100 bp  
9095 9808: contig of 804 bp in length  
9809 9908: gap of 100 bp  
9909 10606: contig of 798 bp in length  
10607 10796: gap of 100 bp  
10797 11599: contig of 794 bp in length  
11601 11690: gap of 100 bp  
11691 12456: contig of 776 bp in length

12457 12566: gap of 100 bp  
12567 13379: contig of 813 bp in length  
13380 13479: gap of 100 bp  
13480 14285: contig of 806 bp in length  
14286 14385: gap of 100 bp  
14386 15176: contig of 791 bp in length  
15177 15276: gap of 100 bp  
15277 16073: contig of 797 bp in length  
16074 16173: gap of 100 bp  
16174 16990: contig of 817 bp in length  
16991 17090: gap of 100 bp  
17091 17904: contig of 814 bp in length  
17905 18004: gap of 100 bp  
18005 18200: contig of 816 bp in length  
18201 18420: gap of 100 bp  
18421 19201: contig of 791 bp in length  
19202 19401: gap of 100 bp  
19402 20577: contig of 776 bp in length  
20578 20677: gap of 100 bp  
20678 21468: contig of 792 bp in length  
21469 21568: gap of 100 bp  
21569 22356: contig of 787 bp in length  
22357 22456: gap of 100 bp  
22457 22556: contig of 795 bp in length  
22558 23351: gap of 100 bp  
23352 24176: contig of 807 bp in length  
24177 24277: gap of 100 bp  
24278 25100: contig of 823 bp in length  
25101 25200: gap of 100 bp  
25201 25999: contig of 799 bp in length  
25999 26099: gap of 100 bp  
26100 26895: contig of 796 bp in length  
26896 26995: gap of 100 bp  
26996 272810: contig of 815 bp in length  
272811 27920: gap of 100 bp  
27921 28721: contig of 811 bp in length  
28722 28821: gap of 100 bp  
28822 29621: contig of 904 bp in length  
29622 29721: gap of 100 bp  
29722 30521: contig of 787 bp in length  
30522 30621: gap of 100 bp  
30622 31321: contig of 859 bp in length  
31322 31477: gap of 100 bp  
31478 32276: contig of 905 bp in length  
32277 32376: gap of 100 bp  
32377 32993: contig of 817 bp in length  
32994 33293: gap of 100 bp  
33294 34100: contig of 807 bp in length  
34101 34200: gap of 100 bp  
34201 34985: contig of 795 bp in length  
34986 35085: gap of 100 bp  
35086 35883: contig of 798 bp in length  
35884 35983: gap of 100 bp  
35984 36780: contig of 797 bp in length  
36781 36880: gap of 100 bp  
36881 37571: contig of 791 bp in length  
37572 37771: gap of 100 bp  
37772 38554: contig of 783 bp in length  
38555 38654: gap of 100 bp  
38655 39441: contig of 787 bp in length  
39442 39541: gap of 100 bp  
39542 40305: contig of 764 bp in length  
40306 40405: gap of 100 bp  
40406 41184: contig of 779 bp in length  
41185 41284: gap of 100 bp  
41285 42094: contig of 810 bp in length  
42095 42194: gap of 100 bp  
42195 42966: contig of 802 bp in length  
42967 42966: gap of 100 bp  
42967 43887: contig of 791 bp in length  
43888 43987: gap of 100 bp  
43988 44775: contig of 788 bp in length  
44776 44875: gap of 100 bp



Tue Feb 20 11:42:51 2001

us-09-226-046-11.rge

Page 16

























[illegible]

XX W00704094-A1.  
PN  
XX  
XX 96-FPR-1997  
PB  
XX 24-JUL-1996 06W0-FK01167.  
XX  
XX 24-JUL-1996 05FF-0009347.  
XX  
XX (AT1F ) AT1F & CIE.  
XX  
XX  
PI Jockers R, Marullo S, Strosberg AD,  
XX  
XX W0112987-122605712.  
XX  
XX P-PSDB: W25926.  
DR  
XX  
XX New nucleic acid encoding functional melanotin receptor of Xenopus -  
PT for screening for potential (anti)opoids useful for e.g. treating  
PT cardiovascular disease and cancer  
XX  
XX  
XX Claim 1, Page 28-29, 62pp; French

Sequences T79063-66 represent novel allelic genes of the Xenopus laevis melanin receptor MEL-1A. The sequences encode proteins which are 55 amino acids shorter than those described in the prior art. Also the last 2-3 terminal amino acids encoded by these sequences are different from the previously known proteins. This sequence is a short form of the novel receptor MEL-1A also known as Mel-1(epsilon). As compared to the long form (T79065), the difference occurs in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The nucleotide sequence was isolated from cDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalling. MEL-1A has been shown to inhibit adenylyl cyclase, but both proteins can modulate intracellular cAMP, e.g. inhibiting its accumulation induced by an inhibitor of phosphodiesterase.

Sequence 1147 bp; 217 A; 234 G; 242 G; 354 T; 0 others.

Query Match	42.5%	Score 451	TP 12	Length 1147
Best Local Similarity	67.18%	Pred. No. 1.7e-104		
Matches 651	Conservative 149	Mismatches 320	Indels 0	Gaps 0

[illegible]



























---













117: cm\_estp16:\*

118: cm\_estp17:\*

119: cm\_estp18:\*

120: cm\_estp19:\*

121: cm\_estp20:\*

122: cm\_estp21:\*

123: cm\_estp22:\*

124: cm\_estp23:\*

125: cm\_estp24:\*

126: cm\_estp25:\*

127: cm\_estp26:\*

128: cm\_estp27:\*

129: cm\_estp28:\*

130: cm\_estp29:\*

131: cm\_estp30:\*

132: cm\_estp31:\*

133: cm\_estp32:\*

134: cm\_estp33:\*

135: cm\_estp34:\*

136: cm\_estp35:\*

137: cm\_estp36:\*

138: cm\_estp37:\*

139: cm\_estp38:\*

140: cm\_estp39:\*

141: cm\_estp40:\*

142: cm\_estp41:\*

143: cm\_estp42:\*

144: cm\_estp43:\*

145: cm\_estp44:\*

146: cm\_estp45:\*

147: cm\_estp46:\*

148: cm\_estp47:\*

149: cm\_estp48:\*

150: cm\_estp49:\*

151: cm\_estp50:\*

152: cm\_estp51:\*

153: cm\_estp52:\*

154: cm\_estp53:\*

155: cm\_estp54:\*

156: cm\_estp55:\*

157: cm\_estp56:\*

158: cm\_estp57:\*

159: cm\_estp58:\*

160: cm\_estp59:\*

161: cm\_estp60:\*

162: cm\_estp61:\*

163: cm\_estp62:\*

164: cm\_estp63:\*

165: cm\_estp64:\*

166: cm\_estp65:\*

167: cm\_estp66:\*

168: cm\_estp67:\*

169: cm\_estp68:\*

170: cm\_estp69:\*

171: cm\_estp70:\*

172: cm\_estp71:\*

173: cm\_estp72:\*

174: cm\_estp73:\*

175: cm\_estp74:\*

176: cm\_estp75:\*

177: cm\_estp76:\*

178: cm\_estp77:\*

179: cm\_estp78:\*

180: cm\_estp79:\*

181: cm\_estp80:\*

182: cm\_estp81:\*

183: cm\_estp82:\*

184: cm\_estp83:\*

185: cm\_estp84:\*

186: cm\_estp85:\*

187: cm\_estp86:\*

188: cm\_estp87:\*

189: cm\_estp88:\*

190: qb\_gss25:\*

191: qb\_gss26:\*

192: qb\_gss27:\*

193: qb\_gss28:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	226.8	20.9	1101	AL341929 Tetraodon
2	192.2	17.7	338	AL284446 Tetraodon
3	156.2	14.4	618	AL132501 Fugu rubr
4	149.2	13.8	1050	AL339370 Tetraodon
5	118.6	10.9	842	AL305461 Tetraodon
6	87.8	8.1	550	AL285460 Tetraodon
7	86.6	8.0	866	AL210810 Tetraodon
8	85.4	7.9	510	BE654347 M-M-A-0
9	82.8	7.6	979	AL279030 Tetraodon
10	80.4	7.4	440	AL234292 Tetraodon
11	75.4	5.9	652	AM663056 h16405.X
12	74.8	6.9	1095	AL524343 h16405.Y
13	74.4	6.8	386	AL341230 Tetraodon
14	70.8	6.5	961	AL457674 h148106.X
15	69.8	6.4	662	BE787874 h1585581
16	69.8	6.4	662	AZ409268 IMC180P17
17	69.8	6.4	662	AL280631 Oryzob03.X
18	69.2	6.4	597	AL139137 Oryzob01.X
19	68.8	6.3	597	AL102402 h469006.X
20	68.8	6.3	753	AL203847 z950602.1
21	66.6	6.1	816	BE270554 h1875372 hK1403.Y
22	66.6	6.1	816	AL178693 Tetraodon
23	64.8	5.9	1027	AL1305573 Tetraodon
24	64.4	5.9	1027	AL1332496 Fugu rubr
25	64.2	5.8	1037	BE605445 h110e05.X
26	63.2	5.8	666	AL280651 Tetraodon
27	63.2	5.9	934	AL234681 Tetraodon
28	63.2	5.9	934	AL234681 Tetraodon
29	61.6	5.7	601	AL10480 Tetraodon
30	61.2	5.6	514	AL130938 Tetraodon
31	60.6	5.6	846	AL14485 Tetraodon
32	59.9	5.5	436	AL175011 Tetraodon
33	59.4	5.5	466	BE668946 h15813.XA
34	59.2	5.5	924	AL237702 Tetraodon
35	59.2	5.5	924	AL237702 Tetraodon
36	58.8	5.4	1028	AL236845 Tetraodon
37	58.6	5.4	915	AL236845 Tetraodon
38	57.8	5.3	805	AL236845 Tetraodon
39	57.8	5.3	805	AL236845 Tetraodon
40	57.8	5.3	805	AL236845 Tetraodon
41	57.2	5.3	740	AL236845 Tetraodon
42	57.2	5.3	740	AL236845 Tetraodon
43	56.8	5.2	482	AL236845 Tetraodon
44	56.8	5.2	482	AL236845 Tetraodon
45	56.4	5.2	559	AL236845 Tetraodon

## ALIGNMENTS

RESULT 1

CNS05KTS/c

LOCUS

DEFINITION

CNS05KTS 1101 bp DNA

042601 of library A from Tetraodon nigroviridis, genomic survey

ACCESSION

AL341929

VERSION

AL341929.1

KEYWORDS

GSS; genome survey sequence.





















•  
•  
•

•

•

•

•

GenCore version 4.5  
Copyright (c) 1994 - 2000 CompuGen Ltd.

OW nucleic - nucleic search, using sw model

Run on: February 19, 2001, 00:54:07 Search time: 3705.49 Seconds  
(without alignments)  
1526.145 Million cell updates/sec

Title: US-09-226-046-15  
Perfect score: 1105  
Sequence: 1 ggaagatcgtgatacaga.....ggcagatgcctctacgctg 1105

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

GenEmbl.\*  
1: gb\_ba1.\*  
2: gb\_ba2.\*  
3: gb\_cm.\*  
4: gb\_cv.\*  
5: gb\_ph.\*  
6: gb\_pl1.\*  
7: gb\_pl2.\*  
8: gb\_pl3.\*  
9: gb\_pr1.\*  
10: gb\_pr2.\*  
11: gb\_pr3.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: em\_hum1.\*  
15: em\_hum2.\*  
16: em\_hum3.\*  
17: em\_in.\*  
18: em\_om.\*  
19: em\_or.\*  
20: em\_ov.\*  
21: em\_pal.\*  
22: em\_ph.\*  
23: em\_pl.\*  
24: em\_ro.\*  
25: em\_sts.\*  
26: em\_sy.\*  
27: em\_un.\*  
28: em\_vl.\*  
29: gb\_ba3.\*  
30: gb\_in1.\*  
31: gb\_in2.\*  
32: gb\_in3.\*  
33: gb\_pl3.\*  
34: gb\_pl4.\*  
35: em\_ba1.\*  
36: em\_ba2.\*  
37: em\_ha1.\*  
38: em\_ha2.\*  
39: em\_ha3.\*  
40: em\_ha4.\*  
41: em\_ha5.\*  
42: em\_ha6.\*  
43: em\_ha7.\*

44: em\_ha8.\*  
45: em\_ha9.\*  
46: em\_ha10.\*  
47: em\_hum3.\*  
48: em\_hum4.\*  
49: em\_hum5.\*  
50: em\_hum6.\*  
51: gb\_pr5.\*  
52: gb\_pr6.\*  
53: gb\_pr7.\*  
54: gb\_ha1.\*  
55: gb\_ha2.\*  
56: gb\_ha3.\*  
57: gb\_ha4.\*  
58: gb\_ha5.\*  
59: gb\_ha6.\*  
60: gb\_ha7.\*  
61: gb\_ha8.\*  
62: gb\_ha9.\*  
63: gb\_ha10.\*  
64: gb\_ha11.\*  
65: gb\_ha12.\*  
66: gb\_ha13.\*  
67: gb\_ha14.\*  
68: gb\_ha15.\*  
69: gb\_ha16.\*  
70: gb\_ha17.\*  
71: gb\_ha18.\*  
72: gb\_ha19.\*  
73: gb\_ha20.\*  
74: gb\_ha21.\*  
75: gb\_ha22.\*  
76: gb\_ha23.\*  
77: gb\_sts1.\*  
78: gb\_sts2.\*  
79: gb\_vl1.\*  
80: gb\_vl2.\*  
81: gb\_pal1.\*  
82: gb\_pal2.\*  
83: em\_ha9.\*  
84: gb\_ha24.\*  
85: gb\_pr8.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1105	100.0	1105	53	HS025341	U25341 Human Melb
2	1105	100.0	1105	81	AP045654	AP045653 Sequence
3	873	79.0	1954	8	AB035972	AB035972 Homo sapi
4	873	79.0	160287	76	AF002371	AF002371 Homo sapi
5	873	79.0	200596	58	AC010891	AC010891 Homo sapi
6	516.2	46.6	741	11	PS057555	PS057555 Phoxopus su
7	516.2	46.6	1104	4	AF184871	AF184871 Phoxopus su
8	483.8	43.8	1085	51	HS014108	HS014108 Human Mel-1
9	483.8	43.8	1085	81	AP026631	AP026631 Sequence
10	480.6	43.5	1050	81	E12845	E12845 rRNA gene
11	470	42.5	1149	3	CA014109	CA014109 Ovis arie
12	470	42.5	1149	81	AB026632	AB026632 Sequence
13	465.2	42.1	1219	3	AF045219	AF045219 Ovis arie
14	440.2	39.8	1062	11	PS014110	PS014110 Phoxopus su
15	439.6	39.7	1152	4	AF184872	AF184872 Phoxopus su
16	433.6	39.2	1503	11	MM052032	MM052032 Mus musc
17	433	39.1	1062	81	AP026632	AP026632 Sequence
18	428.4	38.6	1226	4	GS031921	GS031921 Gallus gall
19	427	38.6	977	11	AF061168	AF061168 Phoxopus su
20	421.2	38.1	935	4	GS030609	GS030609 Gallus gall
21	420.8	38.1	982	11	AF130341	AF130341 Phoxopus su











TITLE  
JOURNAL

## COMMENT

Baldwin, J., Barina, N., Beckerly, R., Boguslavsky, I., Boukhaltier, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collamore, A., Cooke, P., Develiano, K., Dewar, K., Domino, M., Donahue, L., Doyle, M., Ferrer, J., Fitzhugh, W., Forrest, C., Funke, P., Gale, D., Gattad, J., Gargano, S., Grant, G., Hayes, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kahn, L., Karais, A., Klein, J., Lehotzky, T., Liou, C., Locke, K., MacDonald, P., Marquis, N., McKean, P., McKay, A., McKernan, K., McLaughlin, J., Meidrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Petrusak, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, F., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tittell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wymann, D., Ye, W. J., Zimmer, A. and Zody, K.

Direct Submission  
Submitted (08-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Apr 15, 2000 this sequence version replaced g1:564264  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://www.washington.edu/~genetics/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence\_submissions@genome.wi.mit.edu

Project Information

Center project name: 676\_F\_20

Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960721

Consensus quality: 188099 bases at least Q40

Consensus quality: 194083 bases at least Q30

Consensus quality: 194508 bases at least Q20

Insert size: 210000; agarose-ef

Insert size: 198696; sum-of-contigs

Quality coverage: 4.3 in Q20 bases; agarose-ef

Quality coverage: 4.6 in Q20 bases; sum-of-contigs

- \* NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
- \* This record will be updated with the finished sequence, as soon as it is available and the accession number will be preserved.

```

1      1176: contig of 1176 bp in length
*
* 1177 1276: gap of 100 bp
*
* 1277 3998: contig of 2722 bp in length
*
* 4099 4098: gap of 100 bp
*
* 4099 6244: contig of 2146 bp in length
*
* 6245 6344: gap of 100 bp
*
* 6345 11678: contig of 5334 bp in length
*
* 11679 11778: gap of 100 bp
*
* 11779 16551: contig of 4773 bp in length
*
* 16552 16651: gap of 100 bp
*
* 16652 20374: contig of 3688 bp in length
*
* 20375 20439: gap of 100 bp
*
* 20440 23724: contig of 3285 bp in length
*
* 23725 24824: gap of 100 bp
*
* 24825 32156: contig of 8332 bp in length
*
* 32157 32156: gap of 100 bp
*
* 32157 39104: contig of 6867 bp in length
*
* 39105 49203: gap of 100 bp
*
* 49204 45552: contig of 6349 bp in length
*
* 45553 45652: gap of 100 bp
*
* 45653 53242: contig of 7590 bp in length
*
* 53243 53342: gap of 100 bp
*
* 53343 62765: contig of 9423 bp in length
*
* 62766 62866: gap of 100 bp
*
* 62867 73271: contig of 10405 bp in length

```

## FEATURES

## source

```

* 73272 73371: gap of 100 bp
*
* 73372 87308: contig of 1367 bp in length
*
* 87309 87408: gap of 100 bp
*
* 87409 99684: contig of 12276 bp in length
*
* 99685 99784: gap of 100 bp
*
* 99785 111244: contig of 11460 bp in length
*
* 11245 11344: gap of 100 bp
*
* 11345 130640: contig of 19296 bp in length
*
* 130641 130740: gap of 100 bp
*
* 130741 149317: contig of 18577 bp in length
*
* 149318 149417: gap of 100 bp
*
* 149418 171233: contig of 21816 bp in length
*
* 171234 171333: gap of 100 bp
*
* 171334 200596: contig of 29263 bp in length.
Location/Qualifiers
1..200596
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
/clone="RP11-676F20"
/clone_11b="RP11-11 Human Male BAC"
1..1176
/clone="1176"
/note="assembly-fragment"
1277..3998
/note="assembly-fragment"
4099..6244
/note="assembly-fragment"
6345..11678
/note="assembly-fragment"
11779..16551
/note="assembly-fragment"
16652..20374
/note="assembly-fragment"
20440..23724
/note="assembly-fragment"
23725..32156
/note="assembly-fragment"
32157..39104
/note="assembly-fragment"
39105..49203
/note="assembly-fragment"
49204..45552
/note="assembly-fragment"
45553..53242
/note="assembly-fragment"
53243..62765
/note="assembly-fragment"
62766..62866
/note="assembly-fragment"

```

```

BASE COUNT      58351 a 41738 c 41414 g 57186 t 1907 others
ORIGIN

```

```

Query Match      79.0%  Score 873.  DB Seq. Length 200596;
Best Local Similarity 100.0%  Proc. No. 5-2c-136;
Matches 9730  Consistent 0;  Mismatches 0;  Indels 0;  Gaps 0;

```











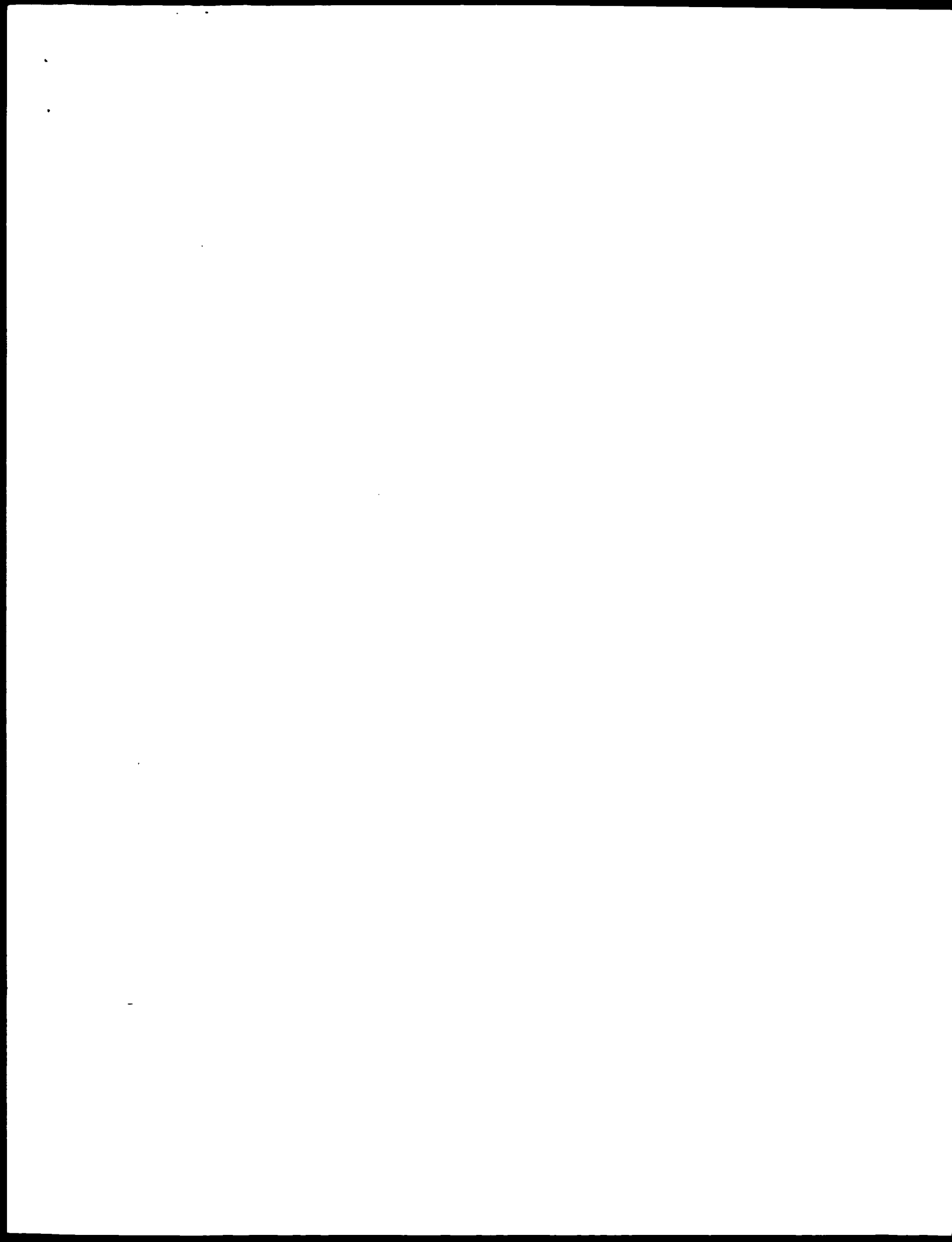














Report SM:  
 WPI: 1996-058168/06.  
 F-PSNM: K88414.  
 DNA encoding high affinity melatonin receptor one - used to identify  
 receptor agonists or antagonists e.g. for regulating circadian  
 rhythm disorders or reproductive cycles  
 Claim 10, Fig 6, 115pp, English.  
 The sequence encodes human high-affinity melatonin-1b receptor,  
 which is a membrane protein, coupled to guanine nucleotide binding  
 proteins (G-proteins), and has been cloned by PCR amplification of  
 human genomic DNA, using primers based on the 3rd and 6th  
 transmembrane domains of the Xenopus sequence (709947), then  
 screening of a human brain cDNA library. The genomic sequence has  
 an intron of about 9.0 kb in the 1st cytoplasmic loop region.  
 Initiation PCR with primers 109953-54 and 43 human rodent somatic  
 cell hybrids has been used to localize the human MNP1b gene to  
 chromosome 11q21-22. Primers 109955-56 and probe 109961 have been  
 used to analyse tissue distribution. Receptor fragments which  
 interact with melatonin, or specific antibodies, may be used as  
 receptor-agonists or receptor-antagonists. Agonists may be used in  
 therapy of circadian rhythm disorders such as jet-lag or day-night  
 cycle disorders, to control ovulation, or in alteration of  
 reproductive cycles in seasonally breeding animals. Antagonists may  
 be used to control the initiation or timing of puberty in humans.  
 The receptor gene may also be expressed in a transgenic animal for  
 use as a model system to screen agonists and antagonists.  
 Sequence 1105 BP: 198 A; 363 G; 303 C; 251 T; 0 other:  
 Query Match 100.0%; Score 1105; DB 17; Length 1105;  
 Best local similarity 100.0%; Freq. No. 2,8e+247;  
 Matches 1105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

541 ttgtgaggtccctgaglaagaccacagcatatctccctgacccctacacagacacg 600  
 541 ttgtgaggtccctgaglaagaccacagcatatctccctgacccctacacagacacg 600  
 601 agcacccagtaacagggagggagtggtgtatccactccctccctccctacagcttctg 660  
 601 agcacccagtaacagggagggagtggtgtatccactccctccctccctacagcttctg 660  
 661 tccctccctacccctgagcatctgagtgagtgagtgagtgagtgagtgagtgagtgagtg 720  
 661 tccctccctacccctgagcatctgagtgagtgagtgagtgagtgagtgagtgagtgagtg 720  
 721 gagagcaggtctgtctgtacagcagcagcagcagcagcagcagcagcagcagcagcagc 780  
 721 gagagcaggtctgtctgtacagcagcagcagcagcagcagcagcagcagcagcagcagc 780  
 781 ttgtgaggtctgtctgtacagcagcagcagcagcagcagcagcagcagcagcagcagc 840  
 781 ttgtgaggtctgtctgtacagcagcagcagcagcagcagcagcagcagcagcagcagc 840  
 841 aaaccccaagaaatggcctcccaaatccctgagagagcagcagcagcagcagcagcagc 900  
 841 aaaccccaagaaatggcctcccaaatccctgagagagcagcagcagcagcagcagcagc 900  
 901 gctatctccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 960  
 901 gctatctccacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 960  
 961 agggatatacaagagagatctctcttgagcctcttgagcagcagcagcagcagcagcagc 1020  
 961 agggatatacaagagagatctctcttgagcctcttgagcagcagcagcagcagcagcagc 1020  
 1021 tccagagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1080  
 1021 tccagagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1080  
 1081 caccagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1105  
 1081 caccagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1105

RESULT 2  
 ID X05747 standard; DNA: 1053 BP.  
 AC X05747;  
 XX  
 XX 28 APR 1999 (first entry)  
 DE Human melatonin receptor mel-1a encoding DNA  
 NE  
 XX Melatonin receptor, mel-1a, human, screening; holmone; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX  
 XX Key location/Qualifiers  
 FT 1..1053  
 FT CDS  
 FT /\*tag= a  
 FT /transl\_except= (pos:745..747, aa:Phe)  
 FT /transl\_except= (pos:820..822, aa:Phe)  
 FT /product= "melatonin receptor mel-1a"  
 PD EP892046-A2.  
 PD 20-JAN-1999.  
 PD 19-JUN-1998; 98EP-0111352.  
 PD 19-JUN-1997; 97JP-0180537.  
 PA (JCEP-) JCR PHARM CO LTD.

























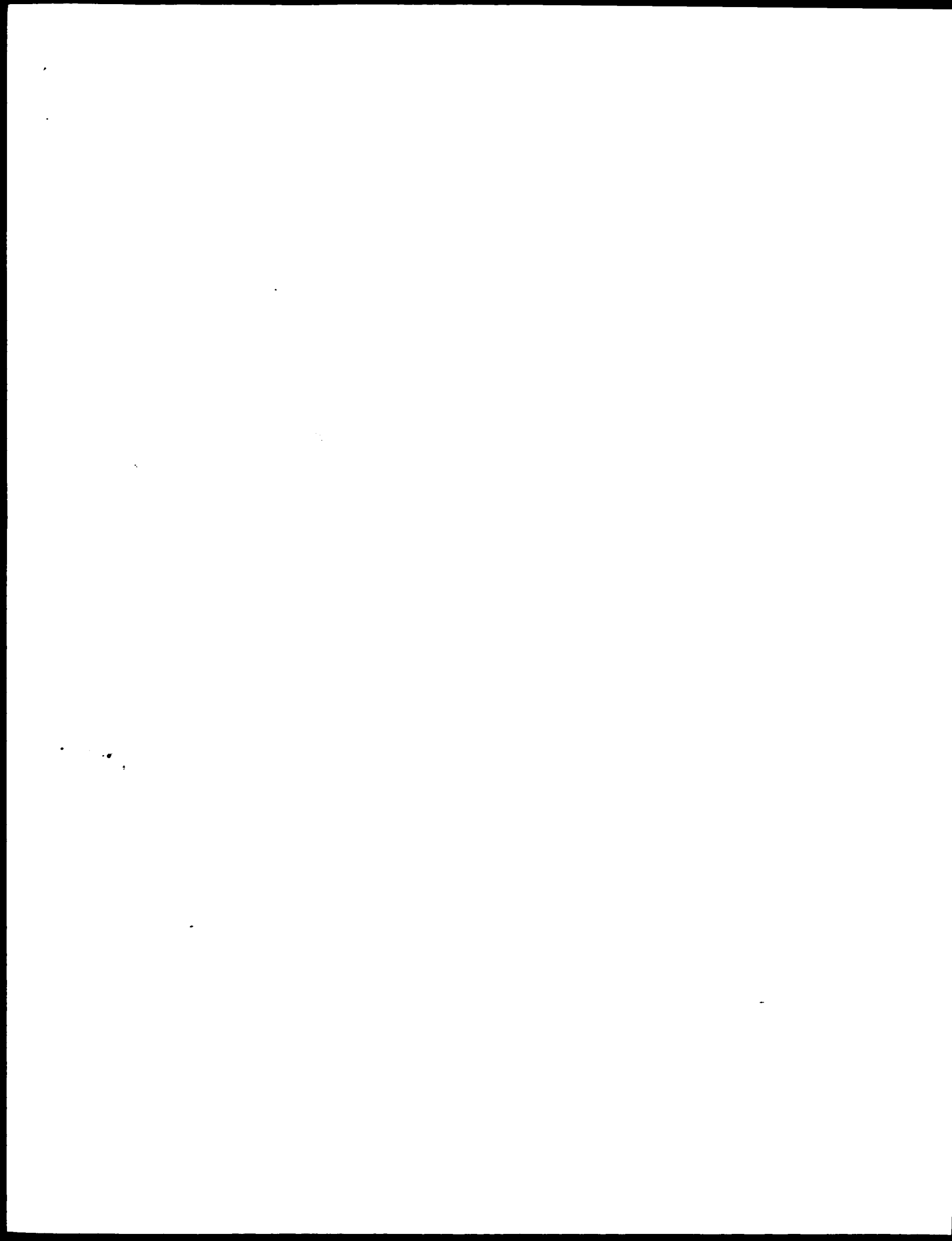




Best Local Similarity 48.38; Pred. No. 5.1e-14;  
Matches 276; Conservative 0; Mismatches 295; Indels 0; Gaps 0;

```
QY 165 cagccgtgagagctgctgaggaacctctctgctgacccctccgtgctcaggaaccggaact 224
    || |||| ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 660 cagggatggagcatcagggcaacctcagcaacctcagcagcagcagcagcagcagcagc 719
    || || || || || || || || || || || || || || || || || || || || || ||
QY 225 ccggaacgaggaatttctctgctgagcctgagcctgagcctgagcctgagcctgagcct 284
    || || || || || || || || || || || || || || || || || || || || || ||
Db 720 agagaccacacacacacacacacacacacacacacacacacacacacacacacacacac 779
    || || || || || || || || || || || || || || || || || || || || || ||
QY 285 ctaccctaccgctaacctcctgagcactctctcagagcctgagcctgagcctgagcct 344
    || || || || || || || || || || || || || || || || || || || || || ||
Db 780 atgcatgagcctgagcctgagcctgagcctgagcctgagcctgagcctgagcctgagc 839
    || || || || || || || || || || || || || || || || || || || || || ||
QY 345 acactgcaagcagcagcctctgagcctgagcctgagcctgagcctgagcctgagcctgag 404
    || || || || || || || || || || || || || || || || || || || || || ||
Db 840 gctctgaggaactctctgagcctgagcctgagcctgagcctgagcctgagcctgagcct 899
    || || || || || || || || || || || || || || || || || || || || || ||
QY 405 cactgacatgagcctaacccgctactgctaacctctgagcagcagcagcagcagcagc 464
    || || || || || || || || || || || || || || || || || || || || || ||
Db 900 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 959
    || || || || || || || || || || || || || || || || || || || || || ||
QY 465 ctgagcagcctgagcctgagcctgagcctgagcctgagcctgagcctgagcctgagc 524
    || || || || || || || || || || || || || || || || || || || || || ||
Db 960 gctacccaagggagcctgagcctgagcctgagcctgagcctgagcctgagcctgagc 1019
    || || || || || || || || || || || || || || || || || || || || || ||
QY 525 ctgctgagcctgagcctgagcctgagcctgagcctgagcctgagcctgagcctgagc 584
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1020 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1079
    || || || || || || || || || || || || || || || || || || || || || ||
QY 585 ctgcatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 644
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1080 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1139
    || || || || || || || || || || || || || || || || || || || || || ||
QY 645 cctatgagcctgagcctgagcctgagcctgagcctgagcctgagcctgagcctgagc 704
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1140 atgagcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1199
    || || || || || || || || || || || || || || || || || || || || || ||
QY 705 cagcaaacccaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 735
    || || || || || || || || || || || || || || || || || || || || || ||
Db 1200 cagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1230
    || || || || || || || || || || || || || || || || || || || || || ||
```

Search completed: February 18, 2001, 20:26:52  
Job time: 13016 sec











```

457 ATTORNEY/AGENT INFORMATION:
472 NAME: Fraser, Janis K.
473 REGISTRATION NUMBER: 34,819
474 REFERENCE/DOCKET NUMBER: 00246/44002
475 TELEPHONE: 617/542-507
476 TELEFAX: 617/542-800
477 TELETYPE: 200154
478 INFORMATION FOR SEQ ID NO: 1:
479 SEQUENCE CHARACTERISTICS:
480 LENGTH: 2772 base pairs
481 TYPE: nucleic acid
482 STANDARDS: single
483 TOPOLOGY: linear
484 FEATURE:
485 NAME/KEY: Coding Sequence
486 LOCATION: 1570..2738
487 OTHER INFORMATION: Intron coding sequence between positions 1449
US-09-290-420-1

```

Query Match 39.2% Score 433.6; DB 2; Length 2772;  
 Post Local Similarity 66.2%; Pred. No. 66-86;  
 Matches 625; Conservative 0; Mismatches 319; Indels 0; Gaps 0;

```

457 ATTORNEY/AGENT INFORMATION:
472 NAME: Fraser, Janis K.
473 REGISTRATION NUMBER: 34,819
474 REFERENCE/DOCKET NUMBER: 00246/44002
475 TELEPHONE: 617/542-507
476 TELEFAX: 617/542-800
477 TELETYPE: 200154
478 INFORMATION FOR SEQ ID NO: 1:
479 SEQUENCE CHARACTERISTICS:
480 LENGTH: 2772 base pairs
481 TYPE: nucleic acid
482 STANDARDS: single
483 TOPOLOGY: linear
484 FEATURE:
485 NAME/KEY: Coding Sequence
486 LOCATION: 1570..2738
487 OTHER INFORMATION: Intron coding sequence between positions 1449
US-09-290-420-1

```

Query Match 39.2% Score 433.6; DB 2; Length 2772;  
 Post Local Similarity 66.2%; Pred. No. 66-86;  
 Matches 625; Conservative 0; Mismatches 319; Indels 0; Gaps 0;

```

457 ATTORNEY/AGENT INFORMATION:
472 NAME: Fraser, Janis K.
473 REGISTRATION NUMBER: 34,819
474 REFERENCE/DOCKET NUMBER: 00246/44002
475 TELEPHONE: 617/542-507
476 TELEFAX: 617/542-800
477 TELETYPE: 200154
478 INFORMATION FOR SEQ ID NO: 1:
479 SEQUENCE CHARACTERISTICS:
480 LENGTH: 2772 base pairs
481 TYPE: nucleic acid
482 STANDARDS: single
483 TOPOLOGY: linear
484 FEATURE:
485 NAME/KEY: Coding Sequence
486 LOCATION: 1570..2738
487 OTHER INFORMATION: Intron coding sequence between positions 1449
US-09-290-420-1

```

Query Match 39.2% Score 433.6; DB 2; Length 2772;  
 Post Local Similarity 66.2%; Pred. No. 66-86;  
 Matches 625; Conservative 0; Mismatches 319; Indels 0; Gaps 0;







Db 451 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 410  
 QY 405 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 464  
 Db 411 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 470  
 QY 465 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 521  
 Db 471 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 530  
 QY 522 GAGC 525  
 Db 531 GCGC 534

RESULT 9  
 PCT-0895-05616-5  
 Sequence 1, Application EC/US9505616  
 GENERAL INFORMATION:  
 APPLICANT: LI, ET AL.  
 TITLE OF INVENTION: Human Neuropeptide Receptor  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CAPPELLA, BYRNE, BAIN, GILFILLAN,  
 ADDRESSEE: CROCH, STEWART & OLSTEIN  
 STREET: 6 BECKER FARM ROAD  
 CITY: ROSELAND  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 INCH DISKETTE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/05616  
 FILING DATE: concurrently  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: FERRARO, GREGORY D.  
 REGISTRATION NUMBER: 36,134  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1133 BASE PAIRS  
 TYPE: NUCLEIC ACID  
 STRANDEDNESS: SINGLE  
 TOPOLOGY: LINEAR  
 MOLECULE TYPE: CDNA  
 PCT-0895-05616-5

Query Match 8.2% Score 90.4, DB 4, Length 1133;  
 Best Local Similarity 54.9% Pred. No. 2e-11;  
 Matches 200; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

QY 165 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 224  
 Db 171 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 230  
 QY 225 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 284  
 Db 231 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 290  
 QY 285 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 344  
 Db 291 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 350

QY 345 GAGCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 404  
 Db 351 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 410  
 QY 405 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 464  
 Db 411 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 470  
 QY 465 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 521  
 Db 471 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 530  
 QY 522 GAGC 525  
 Db 531 GCGC 534

RESULT 10  
 US-08-846-705-1  
 Sequence 1, Application US/08846705  
 Patent No. 5935814  
 GENERAL INFORMATION:  
 APPLICANT: BERGMA, DEBK I  
 TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED  
 NUMBER OF SEQUENCES: 5  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: PATNER & PRESTIA  
 STREET: P.O. BOX 980  
 CITY: VALLEY FORGE  
 STATE: PA  
 COUNTRY: USA  
 ZIP: 19482  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTEST for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/846,705  
 FILING DATE: 30-Apr-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: PRESTIA, PAUL F  
 REGISTRATION NUMBER: 23,031  
 REFERENCE/DOCKET NUMBER: GR-70003  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 610-407-0700  
 TELEFAX: 610-407-0701  
 TELEEX: 846169  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1170 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: CDNA  
 US-08-846-705-1

Query Match 8.2% Score 90.4; DB 2; Length 1170;  
 Best Local Similarity 54.9% Pred. No. 2e-11;  
 Matches 200; Conservative 0; Mismatches 161; Indels 3; Gaps 1;

QY 165 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 224  
 Db 171 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 230  
 QY 225 CCGTCTGCAAGTATATGCGGATCTACAGAGGATGCGGAGCTGCTAACTCT 284

```

DB 231 GAGGACATGACGACTGATTAATGATGAACTGATGAGTGAAGCTTATGATGATGAGT 290
CY 285 CTAACCCGACGCGGCTAACTGCGATGCGCATCTCTGATGAAGGCGCGCGCGGAGGAG 344
DB 291 TATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350
CY 345 GACCTGCAAGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
DB 351 CTTCTGTAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 410
CY 405 CACTGCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
DB 411 CAGCTTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
CY 465 CTAACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 521
DB 471 AGCCCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 530
CY 522 GACCG 525
DB 531 GCCC 534

```

## RESULT 11

```

PCT-US95-05616-1
Sequence 1, Application 67/US9505616
GENERAL INFORMATION:
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Neuropetide Receptor
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, RYRNE, RAIN, GILFILLAN,
ADDRESS: CECCH, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05616
FILING DATE: concurrently
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325900-268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1209 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
PCT-US95-05616-1

```

```

Query Match 82% Score 30.4 DB 4: Length 1209
Best Local Similarity 54.9% Pred. No. 2e-11
Matches 200 Conservative 0 Mismatches 161 Indels 3 Gaps 1

```

```

CY 165 GAGGACATGACGACTGATTAATGATGAACTGATGAGTGAAGCTTATGATGATGAGT 224
DB 171 TATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 230
CY 225 CTAACCCGACGCGGCTAACTGCGATGCGCATCTCTGATGAAGGCGCGCGCGGAGGAG 284

```

```

DB 231 GAGGACATGACGACTGATTAATGATGAACTGATGAGTGAAGCTTATGATGATGAGT 290
CY 285 CTAACCCGACGCGGCTAACTGCGATGCGCATCTCTGATGAAGGCGCGCGCGGAGGAG 344
DB 291 TATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 350
CY 345 GACCTGCAAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
DB 351 CTTCTGTAAGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 410
CY 405 CACTGCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
DB 411 CAGCTTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
CY 465 CTAACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 521
DB 471 AGCCCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 530
CY 522 GACCG 525
DB 531 GCCC 534

```

## RESULT 12

```

US-08-846-705-4
Sequence 4, Application US/08846705
Patent No. 5935814
GENERAL INFORMATION:
APPLICANT: BERGSMAN, DEBK J.
APPLICANT: ELLIS, CATHERINE E
TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: IBM Compatible
SOFTWARE: FASTA for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,705
FILING DATE: 30-Apr-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1564 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-846-705-4

```

```

Query Match 92% Score 66.4 DB 3: Length 1564
Best Local Similarity 54.9% Pred. No. 2.1e-11
Matches 200 Conservative 0 Mismatches 161 Indels 3 Gaps 1

```







Tue Feb 20 11:42:59 2001

us-09-226-046-15.rni

---

Page 12

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

CM nucleic nucleic search, using sw model

Run on: February 18, 2001, 23:47:30 Search time: 1863.01 seconds  
(without alignments)  
4176.726 Million cell updates/sec

Title: US-09-226-046-15

Perfect score: 1105  
Sequence: 1 gggagatgctctgagatgctaga gggagatgctctgagatgctaga 1105

Scoring table: IDENTITY NUC  
Gapop 10 0, Gapext 1 0

Searched: 7691742 seqs, 3503743859 residues

Total number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: qb\_est1:\*\n2: qb\_est2:\*\n3: qb\_est3:\*\n4: qb\_est4:\*\n5: qb\_est5:\*\n6: qb\_est6:\*\n7: qb\_est7:\*\n8: qb\_est8:\*\n9: qb\_est9:\*\n10: qb\_est10:\*\n11: qb\_est11:\*\n12: qb\_est12:\*\n13: qb\_est13:\*\n14: qb\_est14:\*\n15: qb\_est15:\*\n16: qb\_est16:\*\n17: qb\_est17:\*\n18: qb\_est18:\*\n19: qb\_est19:\*\n20: qb\_est20:\*\n21: qb\_est21:\*\n22: qb\_est22:\*\n23: qb\_est23:\*\n24: qb\_est24:\*\n25: qb\_est25:\*\n26: qb\_est26:\*\n27: qb\_est27:\*\n28: qb\_est28:\*\n29: qb\_est29:\*\n30: qb\_est30:\*\n31: qb\_est31:\*\n32: qb\_est32:\*\n33: qb\_est33:\*\n34: qb\_est34:\*\n35: qb\_est35:\*\n36: qb\_est36:\*\n37: qb\_est37:\*\n38: qb\_est38:\*\n39: qb\_est39:\*\n40: qb\_est40:\*\n41: em\_estba:\*\n42: em\_estbm1:\*\n43: em\_estbm2:\*

44: em\_estbm3:\*\n45: em\_estbm4:\*\n46: em\_estbm5:\*\n47: em\_estbm6:\*\n48: em\_estbm7:\*\n49: em\_estbm8:\*\n50: em\_estbm9:\*\n51: em\_estbm10:\*\n52: em\_estbm11:\*\n53: em\_estbm12:\*\n54: em\_estbm13:\*\n55: em\_estbm14:\*\n56: em\_estbm15:\*\n57: em\_estbm16:\*\n58: em\_estbm17:\*\n59: em\_estbm18:\*\n60: em\_estbm19:\*\n61: em\_estbm20:\*\n62: em\_estbm21:\*\n63: em\_estbm22:\*\n64: em\_estbm23:\*\n65: em\_estbm24:\*\n66: em\_estbm25:\*\n67: em\_estbm26:\*\n68: em\_estbm27:\*\n69: em\_estbm28:\*\n70: em\_estbm29:\*\n71: em\_estbm30:\*\n72: em\_estbm31:\*\n73: em\_estbm32:\*\n74: em\_estbm33:\*\n75: em\_estbm34:\*\n76: em\_estbm35:\*\n77: em\_estbm36:\*\n78: em\_estbm37:\*\n79: em\_estbm38:\*\n80: em\_estbm39:\*\n81: em\_estbm40:\*\n82: em\_estbm41:\*\n83: em\_estbm42:\*\n84: em\_estbm43:\*\n85: em\_estbm44:\*\n86: em\_estbm45:\*\n87: em\_estbm46:\*\n88: em\_estbm47:\*\n89: em\_estbm48:\*\n90: em\_estbm49:\*\n91: em\_estbm50:\*\n92: em\_estbm51:\*\n93: em\_estbm52:\*\n94: em\_estbm53:\*\n95: em\_estbm54:\*\n96: em\_estbm55:\*\n97: em\_estbm56:\*\n98: em\_estbm57:\*\n99: em\_estbm58:\*\n100: em\_estbm59:\*\n101: em\_estbm60:\*\n102: em\_estbm61:\*\n103: em\_estbm62:\*\n104: em\_estbm63:\*\n105: em\_estbm64:\*\n106: em\_estbm65:\*\n107: em\_estbm66:\*\n108: em\_estbm67:\*\n109: em\_estbm68:\*\n110: em\_estbm69:\*\n111: em\_estbm70:\*\n112: em\_estbm71:\*\n113: em\_estbm72:\*\n114: em\_estbm73:\*\n115: em\_estbm74:\*\n116: em\_estbm75:\*

117: em\_estp16:\*

118: em\_estp17:\*

119: em\_estp18:\*

120: em\_estp19:\*

121: em\_estp20:\*

122: em\_estp21:\*

123: em\_estp22:\*

124: em\_estp23:\*

125: em\_estp24:\*

126: em\_estp25:\*

127: em\_estp26:\*

128: em\_estp27:\*

129: em\_estp28:\*

130: em\_estp29:\*

131: em\_estp30:\*

132: em\_estp31:\*

133: em\_estp32:\*

134: em\_estp33:\*

135: em\_estp34:\*

136: em\_estp35:\*

137: em\_estp36:\*

138: em\_estp37:\*

139: em\_estp38:\*

140: em\_estp39:\*

141: em\_estp40:\*

142: em\_estp41:\*

143: em\_estp42:\*

144: em\_estp43:\*

145: em\_estp44:\*

146: em\_estp45:\*

147: em\_estp46:\*

148: em\_estp47:\*

149: em\_estp48:\*

150: em\_estp49:\*

151: em\_estp50:\*

152: em\_estp51:\*

153: em\_estp52:\*

154: em\_estp53:\*

155: em\_estp54:\*

156: em\_estp55:\*

157: em\_estp56:\*

158: em\_estp57:\*

159: em\_estp58:\*

160: em\_estp59:\*

161: em\_estp60:\*

162: em\_estp61:\*

163: em\_estp62:\*

164: em\_estp63:\*

165: em\_estp64:\*

166: em\_estp65:\*

167: em\_estp66:\*

168: em\_estp67:\*

169: em\_estp68:\*

170: em\_estp69:\*

171: em\_estp70:\*

172: em\_estp71:\*

173: em\_estp72:\*

174: em\_estp73:\*

175: em\_estp74:\*

176: em\_estp75:\*

177: em\_estp76:\*

178: em\_estp77:\*

179: em\_estp78:\*

180: em\_estp79:\*

181: em\_estp80:\*

182: em\_estp81:\*

183: em\_estp82:\*

184: em\_estp83:\*

185: em\_estp84:\*

186: em\_estp85:\*

187: em\_estp86:\*

188: em\_estp87:\*

189: em\_estp88:\*

190: qb\_gss25:\*

191: qb\_gss26:\*

192: qb\_gss27:\*

193: qb\_gss28:\*

Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	185.8	16.8	938	192	CNS04CH1	AL284446 Tetradon
2	181.4	16.4	1101	193	CNS04CH1	AL341925 Tetradon
3	123.9	11.1	842	192	CNS04SOS	AL304461 Tetradon
4	113	10.2	1050	193	CNS04SOS	AL319370 Tetradon
5	109.8	9.9	1014	193	PR0045009	AL132501 Fugu rubr
6	90	7.2	1014	193	CNS04SOS	AL165749 Tetradon
7	79.8	7.2	938	192	CNS04SOS	AL118810 Tetradon
8	79.8	7.2	938	192	CNS04SOS	AL118810 Tetradon
9	79.8	7.2	440	93	AW643056	AW643056 h14305.x
10	79.8	7.2	440	93	AW643056	AW643056 h14305.x
11	76.4	6.9	646	192	CNS04SOS	AL280651 Tetradon
12	76.4	6.9	386	20	AL1457674	AL1457674 h148106.x
13	72.4	6.5	510	111	BE654347	BE654347 UT-M-A00-
14	71.4	6.5	979	192	CNS04SOS	AL285640 Tetradon
15	71.2	6.4	618	193	PR0040608	AL128101 Fugu rubr
16	71.2	6.4	785	193	CNS04SOS	AL175011 Tetradon
17	69.6	6.3	1095	193	CNS05KAD	AL341230 Tetradon
18	66.4	6.0	688	26	AL1875272	AL1875272 h131d03.y
19	65.8	6.0	566	111	BE668896	BE668896 159318 MA
20	65	5.9	938	192	CNS03S2M	AL2858205 Tetradon
21	64.2	5.8	652	26	AL1929243	AL1929243 h159009.y
22	63.8	5.8	916	191	CNS04S2X	AL14406 Tetradon
23	63.8	5.7	529	93	AW653917	AW653917 102840 MA
24	62.8	5.7	529	93	AW653917	AW653917 102840 MA
25	61.8	5.6	984	192	CNS04S2M	AL239897 Tetradon
26	61.8	5.6	1033	190	CNS0138N	AL237173 Tetradon
27	60.6	5.5	965	192	CNS0309V	AL165028 Tetradon
28	60.4	5.5	732	106	BE379625	AL258676 Tetradon
29	60.4	5.5	846	192	CNS038PA	AL260119 Tetradon
30	59.4	5.4	753	23	AL623442	AL623442 h459d06.x
31	59.4	5.4	1037	193	CNS02V02	AL177409 Tetradon
32	58.8	5.3	910	190	CNS0080N	AL065629 Orosophillu
33	58	5.2	562	144	BE045009	AL065629 Orosophillu
34	57.8	5.2	520	39	AW077212	AW077212 133219 MA
35	57.6	5.2	599	46	AW106831	AW077212 h133309.y
36	57.6	5.2	896	191	CNS03S2M	AW106831 h143305.y
37	57.2	5.2	818	192	CNS03S2M	AL237689 Tetradon
38	57.2	5.2	824	127	BE903653	AL245689 Tetradon
39	57	5.2	865	137	BE903653	BE903715 6016753727
40	56.2	5.1	805	191	CNS03C0L	AL237702 Tetradon
41	56	5.1	679	18	AL353895	AL253985 SAL026 BL
42	56	5.1	679	18	AL353895	AL253985 Tetradon
43	55.8	5.0	340	68	AW281299	AW281299 h152103.y
44	55.8	5.0	1070	192	CNS03S2M	AL258742 Tetradon
45	55.2	5.0	1476	93	AW643073	AW643073 h14305.x

## ALIGNMENTS

RESULT 1

CNS04CH1 636 bp TNA

DEFINITION

099D15 of library G from Tetradon nigroviridis genome survey sequence.

ACCESSION

AL284446

VERSION

AL284446.1

KEYWORDS

GSS: genome survey sequence.

21 MAY-2000

















```

257 149cattatgacacgctgagctgagcctctacccctacccgctacccctctgagccatct 316
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
410 tccgcattgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
417 tctatgacacgctgagcctgagcctgagcctgagcctgagcctgagcctgagcctg 376
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
460 tccgcattgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 391
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
477 tctatgacacgctgagcctgagcctgagcctgagcctgagcctgagcctgagcctg 436
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
490 tctatgacacgctgagcctgagcctgagcctgagcctgagcctgagcctgagcctg 444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
497 tctatgacacgctgagcctgagcctgagcctgagcctgagcctgagcctgagcctg 456
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
510 tctatgacacgctgagcctgagcctgagcctgagcctgagcctgagcctgagcctg 468
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
517 tctatgacacgctgagcctgagcctgagcctgagcctgagcctgagcctgagcctg 476
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
520 tctatgacacgctgagcctgagcctgagcctgagcctgagcctgagcctgagcctg 484
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
527 tctatgacacgctgagcctgagcctgagcctgagcctgagcctgagcctgagcctg 492
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
530 tctatgacacgctgagcctgagcctgagcctgagcctgagcctgagcctgagcctg 500
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 14
CONS04107 560 bp ENA GSS 21-MAY-2000
LOCUS Tetraodon nigroviridis genome survey sequence 57 and 61 clone
DEFINITION 130522 of library 5 from Tetraodon nigroviridis; genome survey
sequence.
ACCESSION AL285640
VERSION AL285640.1
KEYWORDS GSS: genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis.

```

```

REFERENCE 1 (bases 1 to 550)
AUTHORS Bonnet-Aud, P., Billault, A., Querlet, F., Saurin, W., Bernot, A. and
Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater puterfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 550)
AUTHORS Bonnet-Aud, P., Billault, A., Querlet, F., Saurin, W., Bernot, A.,
Fisher, C.,
Weissenbach, J.
TITLE Human genome number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 550)
AUTHORS Bonnet-Aud, P., Billault, A., Querlet, F., Saurin, W., Bernot, A.,
Fisher, C.,
Weissenbach, J.
TITLE Human genome number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished

```

```

FEATURES
Source
Location/Qualifiers
1..550
/organism="Tetraodon nigroviridis"
/db_xref="taxon 9684"
/seq_id="1000000"

```

```

Query Match 6.58: Score 71.4; DB 193; Length 550;
Best Local Similarity 54.4%; Fred No. 2,260,071;
Matches 142; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
BASE COUNT 114 a 157 c 166 g 99 t 14 others
ORIGIN
1..550
/organism="Tetraodon nigroviridis"
/db_xref="taxon 9684"
/seq_id="1000000"

```

```

RESULT 15
PRO0040608/c 618 bp ENA GSS 22-OCT-1999
LOCUS Fugu rubripes GSS sequence, clone 122112b10, genome survey
sequence.
DEFINITION Fugu rubripes GSS sequence, clone 122112b10, genome survey
sequence.
ACCESSION AL128101
VERSION AL128101.1
KEYWORDS GSS: genome survey sequence.
SOURCE Fugu rubripes.
ORGANISM Fugu rubripes.

```

```

REFERENCE 1 (bases 1 to 618)
AUTHORS Umetani, Y., Williams, J., Smith, S., Meek, S., Warner, J., Edwards, Y., J. K.,
and Brenner, S.
TITLE Direct Submission
JOURNAL Submitted (11-OCT-1999) MRC Human Genome Mapping Project Resource
Centre, Hinxton, Cambridgeshire, CB10 1SB, UK Email:
bioinformatics@hmp.mrc.ac.uk
Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
DESCR:
The Fugu rubripes genome survey sequence of clone 122112b10, genomic
sequence.

```

```

FEATURES
Source
Location/Qualifiers
1..618
/organism="Fugu rubripes"
/db_xref="taxon 31033"
/clone_lib="cosmid.122112"
/clone="122112b10"
BASE COUNT 100 a 152 c 194 g 104 t 68 others
ORIGIN
1..618
/organism="Fugu rubripes"
/db_xref="taxon 31033"
/clone_lib="cosmid.122112"
/clone="122112b10"

```

```

Query Match 6.48: Score 71.2; DB 193; Length 618;
Best Local Similarity 54.4%; Fred No. 2,260,071;
Matches 142; Conservative 0; Mismatches 119; Indels 0; Gaps 0;
BASE COUNT 114 a 157 c 166 g 99 t 14 others
ORIGIN
1..618
/organism="Fugu rubripes"
/db_xref="taxon 31033"
/clone_lib="cosmid.122112"
/clone="122112b10"

```

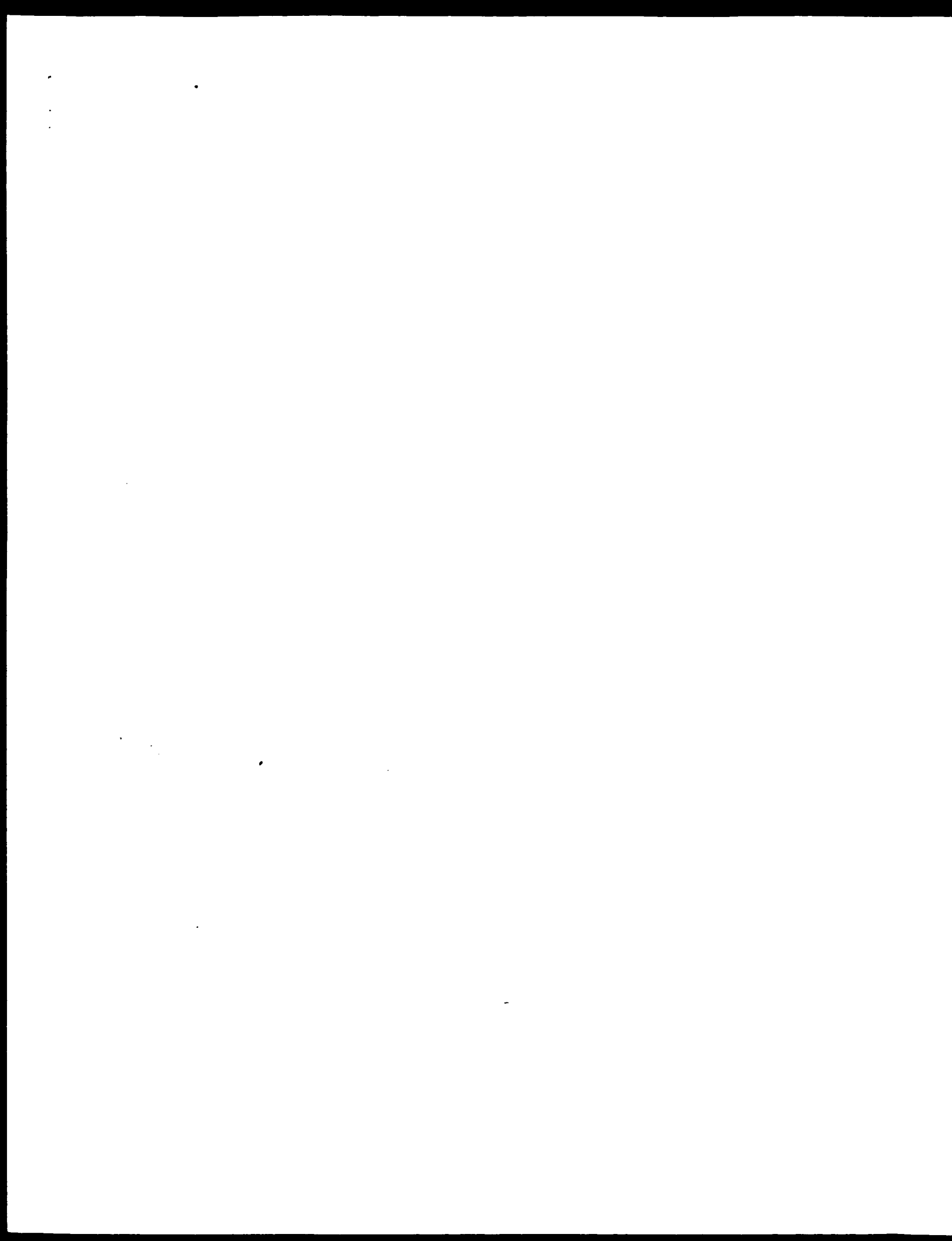
Tue Feb 20 11:43:00 2001

us-09-226-046-15.rst

Page 11

[illegible]

Search completed: February 18, 2001, 23:47:45  
Job time: 16009 sec



GenCore version 4.5  
Copyright 1991-1999 GenCorp Inc

DM protein - protein search, using sw model

February 18 2001 20:19:12 Search time 72.17 seconds

(Without alignments)  
171,514 Million bits of data were

US-09-226-046-16

Perfect score:

1908

EMISS=11.11, HMM=11.11

Sequence:

1 MGENGFANVGFAGTWAVE

Scoring table:

BL0SUM62

Gapop 10.0 , Gapext 0.5

Database:

26485 seqs, 1413035 residues

Total number of hits satisfying chosen parameters

768485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

A\_Geneseq\_362

1: /cnr2\_2/gcadata/geneseq/AA1980.DAT

2: /cnr2\_2/gcadata/geneseq/AA1981.DAT

3: /cnr2\_2/gcadata/geneseq/AA1982.DAT

4: /cnr2\_2/gcadata/geneseq/AA1983.DAT

5: /cnr2\_2/gcadata/geneseq/AA1984.DAT

6: /cnr2\_2/gcadata/geneseq/AA1985.DAT

7: /cnr2\_2/gcadata/geneseq/AA1986.DAT

8: /cnr2\_2/gcadata/geneseq/AA1987.DAT

9: /cnr2\_2/gcadata/geneseq/AA1988.DAT

10: /cnr2\_2/gcadata/geneseq/AA1989.DAT

11: /cnr2\_2/gcadata/geneseq/AA1990.DAT

12: /cnr2\_2/gcadata/geneseq/AA1991.DAT

13: /cnr2\_2/gcadata/geneseq/AA1992.DAT

14: /cnr2\_2/gcadata/geneseq/AA1993.DAT

15: /cnr2\_2/gcadata/geneseq/AA1994.DAT

16: /cnr2\_2/gcadata/geneseq/AA1995.DAT

17: /cnr2\_2/gcadata/geneseq/AA1996.DAT

18: /cnr2\_2/gcadata/geneseq/AA1997.DAT

19: /cnr2\_2/gcadata/geneseq/AA1998.DAT

20: /cnr2\_2/gcadata/geneseq/AA1999.DAT

21: /cnr2\_2/gcadata/geneseq/AA2000.DAT

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1908	100.0	362	17	High-affinity mel
2	1142	59.9	354	18	Xenopus melatonin
3	1123	58.9	470	17	High-affinity mel
4	1120	58.7	354	18	Xenopus melatonin
5	1088	57.0	350	17	High-affinity mel
6	1088	56.7	350	18	Xenopus melatonin
7	1081	56.7	350	20	Human melatonin re
8	1072.5	55.9	353	19	Mouse melatonin la
9	1066.5	55.9	353	17	High-affinity mel
10	1048	54.9	366	17	High-affinity mel
11	989.5	46.6	288	17	High-affinity mel
12	340.5	17.8	383	14	Sequence of human

13	340	17.8	384	14	R35493	Human NPY receptor
14	340	17.8	384	14	R35494	Human NPY receptor
15	339	17.8	476	17	W03014	Modified neuropept
16	337.5	17.7	411	17	W03012	Neuropeptide Y rec
17	337	17.7	382	17	W02101	Mouse neuropeptide
18	332	17.4	430	21	Y79476	Human neuropeptide
19	332	17.3	428	21	Y56887	Human neuropeptide
20	329.5	17.3	371	17	W02099	Mouse neuropeptide
21	329.5	17.3	399	17	W03013	Modified neuropept
22	325	17.0	441	21	Y34433	Human secretin pro
23	322.5	16.9	432	21	Y79473	Rat neuropeptide F
24	321.5	16.9	432	21	Y56886	Rat B5 receptor po
25	321	16.8	370	20	W97421	Human pituitary G-
26	321	16.8	370	20	W97421	Human pituitary de
27	321	16.8	370	20	W97421	Human G-protein co
28	321	16.8	370	20	W97421	Consensus human hy
29	321	16.8	366	18	W27510	Rat galanin recept
30	318.5	16.7	346	20	Y45129	Human somatostatin
31	318.5	16.7	391	24	R32529	Human G-coupled-pr
32	317	16.6	370	21	Y87805	Human G-coupled-pr
33	314.5	16.5	391	24	R32529	Neuropeptide Y/pep
34	313	16.4	375	16	R79119	Human G-coupled-pr
35	312.5	16.4	369	21	Y87506	Human G-coupled-pr
36	312.5	16.3	369	24	R32529	Marine somatostat
37	310.5	16.3	444	21	Y68888	A murine mu-opioid
38	308	16.1	515	21	Y67736	Mouse alpha-1b adr
39	307.5	16.1	349	16	R79443	Galanin receptor
40	307.5	16.1	349	17	R50970	Human galanin rece
41	307	16.1	515	15	R70995	Human/rat alpha-1b
42	307	16.1	515	16	R90041	Human/rat hybrid a
43	306	16.0	390	16	R56738	Marine adipogenic
44	306	16.0	400	16	R54922	Marine beta-3 adre
45	306	16.0	517	21	Y57193	Sequence of human

#### ALIGNMENTS

RESULT 1	
R88414	16-AUG-1996 (first entry)
ID	R88414 standard; Protein: 362 AA.
XX	
AC	R88414.
DE	High-affinity melatonin-1b receptor.
XX	
DE	Melatonin-1b receptor, human; G-protein-coupled receptor;
XX	cytochrome-c family home binding site; antibody; glycosylation;
KW	melatonin receptor antagonist; melatonin receptor antagonist;
KW	circadian rhythm disorder; jet-lag; day-night cycle disorder;
KW	ovulation, reproductive cycle; animal breeding; puberty;
KW	transgenic animal; drug screening.
OS	Homo sapiens.
XX	
EH	Key
FT	Domain
FT	Modified-site
FT	Location/Qualifiers
FT	1..40
FT	/note= "Extracellular domain"
FT	41..65
FT	/note= "N-glycosylation site"
FT	66..76
FT	/note= "Transmembrane region-1"
FT	77..80
FT	/note= "Intracellular loop"
FT	81..101
FT	/note= "Conserved melatonin receptor motif"
FT	102..115
FT	/note= "Transmembrane region-1"
FT	116..134
FT	/note= "Extracellular loop"
FT	Domain

[illegible]

CY	I	MSEKDSFANCTGNOAAVETQWGSINSGSPSSPTPPPWVAALASAVLIVTAVVNTLL	60
CU	I	MSKGGSLDNDGAGQMAVTPFWQSJASLSILPFFWQJASLSLITLVDFGQSTI	60
EZ	1	MSKGGSLDNDGAGQMAVTPFWQSJASLSILPFFWQJASLSLITLVDFGQSTI	60
F7	61	VHLSVLPNPFESNAQLIVSACALGVAVPYPTVVATFTFGAALGEHGNSAYM	120
F8	62	VHLSVLPNPFESNAQLIVSACALGVAVPYPTVVATFTFGAALGEHGNSAYM	120
F9	63	VHLSVLPNPFESNAQLIVSACALGVAVPYPTVVATFTFGAALGEHGNSAYM	120
G7	101	GVSVGSEVENTAINPCVCYCHSMAPHPYPWPWTPIHQIIMLTVALIPPEVS	180
G8	102	GVSVGSEVENTAINPCVCYCHSMAPHPYPWPWTPIHQIIMLTVALIPPEVS	180
G9	181	LEVDPRYSSTPLQASTGYTAADVIFELDLAVNSFCYLRIWIVLQARKAPERSI	240
H6	191	LQGLPLYSSTGLQASTGYTAADVIFELDLAVNSFCYLRIWIVLQARKAPERSI	240
H7	241	CLMFPSLRLENEMVVFVFAIAQAFNLTLAVAHVDEMAVLPEDLPYSTLAYFN	300
H8	242	CLMFPSLRLENEMVVFVFAIAQAFNLTLAVAHVDEMAVLPEDLPYSTLAYFN	300
OY	301	SCLNAVYGLLNENFEERKYHLHMWNPAHDIQASKASHARISGARHIDVGRAR	360
U6	301	SCLNAVYGLLNENFEERKYHLHMWNPAHDIQASKASHARISGARHIDVGRAR	360
OY	361	AL 362	
DB	361	al 362	
RESULT	2		
M25927			
IC	M25927 standard; Protein: 354 AA.		
XX	M25927;		
AC			
XX			
DT	10-NOV-1997 (first entry)		
EE	Xenopus melatonin receptor MEL-1AB.		
XX			
KW	Allele: Xenopus laevis; melanin; receptor; untranslated leader; PCR;		
KW	mRNA; half-lives; skin amplification primer; polymerase chain reaction;		
KW	membrane domain; cellular signalling; inhibition; decylvi cyclase;		
KW	mutation; intracellular; cyclic GMP; inhibition; phosphodiesterase.		
OS	Xenopus laevis.		
XX			
HH	Key	Location/Qualifiers	
EH	Domain	1..32	
F1	Domain	/note= "Extracellular N-terminal domain"	
EH	Domain	33..56	
EH	Domain	/note= "transmembrane domain 1"	
EH	Domain	57..68	
EH	Domain	/note= "intracellular domain 1"	
EH	Domain	69..92	
EH	Domain	/note= "transmembrane domain 2"	
EH	Domain	93..107	
EH	Domain	/note= "extracellular domain 2"	
EH	Domain	108..125	
EH	Domain	/note= "transmembrane domain 3"	
EH	Domain	126..151	
EH	Domain	/note= "intracellular domain 2"	
EH	Domain	152..171	
EH	Domain	/note= "transmembrane domain 4"	
EH	Domain	172..193	
EH	Domain	/note= "extracellular domain 3"	
EH	Domain	194..219	
EH	Domain	/note= "transmembrane domain 5"	
EH	Domain	220..243	
EH	Domain	/note= "intracellular domain 3"	
EH	Domain	244..268	
EH	Domain	/note= "transmembrane domain 6"	
EH	Domain	269..280	
EH	Domain	/note= "extracellular domain 4"	



FT Domain 281..301  
 FT /note= "transmembrane domain 7"  
 FT 302..354  
 FT Domain /note= "intracellular C-terminal domain"  
 XX  
 XX W09704094-A1.  
 XX  
 XX  
 XX 06-FEB-1997.  
 XX  
 XX 24-JUL-1996: 96WO-FR01167.  
 XX  
 XX 24-JUL-1995: 95FP-0008947.  
 XX  
 XX (ADIR ) ADIR 5 CIE.  
 XX  
 XX Jockers R, Maluio S, Strusberg Ad;  
 XX  
 XX WPI: 1997-132635/12.  
 XX N-PSDB: T79065-6.  
 XX  
 XX New nucleic acid encoding functional melatonin receptor of Xenopus  
 PT for screening for potential (ant)agonists useful for e.g. treating  
 PT cardiovascular disease and cancer  
 PT  
 XX  
 XX Claim 5: Page 30-31; 62pp: French.  
 XX  
 XX Sequences W25926-7 represent novel allelic Xenopus laevis melatonin  
 CC receptor MEL-1A proteins. This sequence is a new form of the melatonin  
 CC receptor designated MEL-1ab, also known as Mel-1c(beta). The protein  
 CC differs from previously known receptors by being 65 amino acids shorter  
 CC and also differs throughout the sequence by 6 amino acids. The protein  
 CC is encoded by 2 different alleles (T79065-6) which differ in the 3'  
 CC untranslated region (both sequences encode the same protein), which is  
 CC thought to affect the half-life of the mRNA. The coding sequence was  
 CC isolated from cDNA derived from Xenopus skin RNA and amplified using the  
 CC primers T79067-76. The nucleotide sequence encodes a 7 transmembrane  
 CC receptor involved in cellular signalling. MEL-1ab has been shown to  
 CC modulate intracellular cGMP, esp. inhibiting its accumulation induced by  
 CC an inhibitor of phosphodiesterase, but unlike the MEL-1A protein, it  
 CC cannot inhibit adenylyl cyclase activity.  
 CC  
 CC Sequence 354 AA:  
 SQ

Query Match 59.98; Score 1142; DB 18; Length 354;  
 Best Local Similarity 60.08; Prod. No. 2.2e-119;  
 Matches 216; Conservativa 79 Mismatches 75; Indels 10; Gaps 3

QY 1 MENSFANCCACGAVRPMWSQNSAPRSTPRPWAFALSAVLIVAVVNNL 60  
 DB 2 TNNSTGIDGTPR--TITGQDQDSTAGQI\* ---SALVWVLTGIVWQVPTL 52  
 QY 51 VILSVLRNRKRLNAGNIFLVSLADLVAAVFPYPLILVAFYDGMALGEECKASAFV 120  
 DB 53 VILSVLRNRKRLNAGNIFLVSLADLVAAVFPYPLILVAFYDGMALGEECKASAFV 120  
 QY 121 GLSVGSFNTAIAINVCYTHGMAHYFIPRMHTLHGLTILVTLVALLNPFVSS 150  
 DB 113 GLSVGSFNTAIAINVCYTHGMAHYFIPRMHTLHGLTILVTLVALLNPFVSS 150  
 QY 181 LEYDPRITSCFTQTASTQYTAAVVIFELPRAVSCYPTIVWLQAPRKAPESPL 240  
 DB 173 LQDPRITSCFTQTASTQYTAAVVIFELPRAVSCYPTIVWLQAPRKAPESPL 240  
 QY 241 CLKPSDLRSTIMVAVFPAICWAPLNTGLIAVINDQENAPQIPGSELVTSLLAVFN 300  
 DB 239 CLKPSDLRSTIMVAVFPAICWAPLNTGLIAVINDQENAPQIPGSELVTSLLAVFN 300  
 QY 301 SLTNIVATLNNFFFEYFTILAKMPRHITLAKLSHAEELSAFAPILVHQAQ 353  
 DB 293 SLTNIVATLNNFFFEYFTILAKMPRHITLAKLSHAEELSAFAPILVHQAQ 353

RESULT 3  
 R88409  
 ID R88409 standard: Protein; 420 AA.  
 XX  
 XX R88409:  
 AC  
 XX 15-AUG-1996 (first entry)  
 XX  
 XX High-affinity melatonin receptor.  
 XX  
 XX Melatonin receptor: G-protein-coupled receptor; glycosylation;  
 XX disulfide bond; ligand binding pocket; phosphorylation;  
 XX cytochrome-c family heme binding site; melatonin receptor-agonists;  
 XX melatonin receptor-antagonists; circadian rhythm disorder; jet-lag;  
 XX day-night cycle disorder; ovulation; reproductive cycle; antibody;  
 XX animal breeding; puberty; transgenic animal; drug screening.  
 XX  
 XX Xenopus laevis.  
 OS  
 XX  
 XX Key  
 FH Location/Qualifiers  
 FH 1..32  
 FH Domain  
 FT /note= "Extracellular domain"  
 FT 5..17  
 FT Modified-site  
 FT /note= "N-glycosylation site"  
 FT 16  
 FT Modified-site  
 FT /note= "Protein-kinase-C phosphorylation site"  
 FT 33..57  
 FT Domain  
 FT /note= "Transmembrane region-I"  
 FT 57..68  
 FT Domain  
 FT /note= "Intracellular loop"  
 FT 67..72  
 FT Region  
 FT /note= "Conserved melatonin receptor motif"  
 FT 69..93  
 FT Domain  
 FT /note= "Transmembrane region-II"  
 FT 94..107  
 FT Domain  
 FT /note= "Extracellular loop"  
 FT 105..182  
 FT Disulfide-bond  
 FT 108..126  
 FT Domain  
 FT /note= "Transmembrane region-III"  
 FT 125..131  
 FT Region  
 FT /note= "Region used to construct primer"  
 FT 127..151  
 FT Domain  
 FT /note= "Intracellular loop"  
 FT 132..137  
 FT Region  
 FT /note= "Putative cytochrome-c family heme binding site"  
 FT 137  
 FT Modified-site  
 FT /note= "Protein-kinase-C phosphorylation site"  
 FT 152..171  
 FT Domain  
 FT /note= "Transmembrane region-IV"  
 FT 166  
 FT Misc-difference  
 FT /note= "Residue which may form ligand binding pocket"  
 FT 172..193  
 FT Domain  
 FT /note= "Extracellular loop"  
 FT 194..220  
 FT Domain  
 FT /note= "Transmembrane region-V"  
 FT 204  
 FT Misc-difference  
 FT /note= "Residue which may form ligand binding pocket"  
 FT 221..243  
 FT Domain  
 FT /note= "Intracellular loop"  
 FT 244..268  
 FT Domain  
 FT /note= "Transmembrane region-VI"  
 FT 252..259  
 FT Region  
 FT /note= "Region used to construct primer"  
 FT 258  
 FT Misc-difference  
 FT /note= "Residue which may form ligand binding pocket"  
 FT 269..279  
 FT Domain  
 FT /note= "Extracellular loop"  
 FT 280..301  
 FT Domain  
 FT /note= "Transmembrane region-VII"  
 FT 296..300  
 FT Region  
 FT /note= "Conserved melatonin receptor motif"  
 FT 302..420  
 FT Domain  
 FT /note= "Intracellular domain"







```

FT      Misc-difference 249          /note- "encoded by ATG"
ET      Misc-difference 274          /note- "encoded by GAG"
FT      FT
XX      EP892046-A2.
XX      FN
XX      PD    20-JAN-1999.
XX      FR
EE      19-JUN-1998:   98EP-0111352.
XX      FR
FR      19-JUN-1997:   97JP-0180537.
XX      PA
PA      (JCRP-) JCR PHARM CO LTD.
XX      PI
PI      Kota J. Shirono H. Yokoyama T.
XX      DR
DR      WPI: 1999-083563/08.
DR      N-PSDB: X05747.
XX      XX
XX      New melatonin-receptor expression cells - useful for screening for
XX      human melatonin receptor proteins and agonists and antagonists
XX      Examples; Fig 2: 2app: English.
XX      XX
XX      This represents a human melatonin receptor mel-1a. The invention
XX      provides materials for screening for a substance showing affinity for a
XX      melatonin receptor protein, which comprises an animal cell containing an
XX      expression plasmid for the gene encoding a human melatonin receptor
XX      protein. The cells are useful for screening for human melatonin receptor
XX      proteins and its antagonist or antagonist e.g. hormones and synthetic
XX      compounds, by measuring changes in metabolic activity. The recombinant
XX      human melatonin receptor protein is useful as it has the same activity as
XX      natural human melatonin receptor protein. The new screening method is
XX      better than prior art radioimmunoassay techniques at quantitatively
XX      determining melatonin, which uses antibodies produced by linking
XX      melatonin to a carrier.
XX      Sequence     350 AA:
SJ
Query Match           56 % Score 1081; DR 20; Length 350;
Rest Local Similarity 60.6%; Pied No. 1,4e-112;
Matches 203; Conservative 53; Mismatches 71; Indels 8; Gaps 1
CQ      24 GAGGAPSPPT-----PPPWVAALCAVLVTAVTAVVGNLIVTSVFENRPFENAG 75
        ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
DQ      3 dngsalpnasgprlqdgarpwlnalaaavlffvvdnlgnllvtlsyrrckklnag 62
CQ      76 NLFLVSLALNLVAAFPYPLLIIVAFIFCDMALFEHCKASFFWGLSVISVSNITIA 139
        ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
DQ      63 nlflvsalavallvaipylvlmsltmrmwngynogvasdlngslsvisnltia 122
CQ      136 INRCVCIOSHNAVRIRFRWHPHLCILMLLVALLPNFVGSLKEDPRIVSCIFIOT 195
        ||||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
DQ      123 inrcvcichshnavrfrwhphlclmlllvlllpnfvgslkedprivscifiot 193
        ||||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
CQ      196 ASTOTTAVVVIHLLLIAVSCFYLPIMVLIQAARPKKPSGLCPSPLSLFIMPV 266
        ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
DQ      183 assyttaavvvhllliaavscfyfplmvliqaarkpkpsglcpspslsfimpv 242
        ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
CQ      256 VEVFAIDMAVLTNIGLAVALINPEWAACPELEVTSTLYAENSCLNAVYSCLNN 315
        ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | :
DQ      243 vevfaidmavltnglavalinpewaacpelevtstlyyensclnavysclnn 302
        ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | :
CQ      316 PREYKPILLAIWNPBCITGLASKGSNAEDLNQAP 350
        ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | :
DQ      303 preykpillaiwnpbctglaskgsnaedlnqap 337
        ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | : ||||| | :

RESULT      8
W23958 standard: Protein: 351 AA.
ID      W23958
```

XX	AC		W23958;	
XX	DI	06-JUL-1998	(first entry)	
XX	DE		Mouse melatonin 1a receptor.	
XX	KM		Melatonin 1a receptor. Mel1a gene; circadian rhythm; puberty; reproductive cycle; jet lag; mouse; G-protein coupled receptor.	
XX	OS		Mus musculus.	
XX	FH	Key	Location/Qualifiers	
FT		Modified-site	4..6	
FT		/note= "Asn is N-glycosylated"		
FT		Modified-site	10..12	
FT		/note= "Asn is N-glycosylated"		
FT		Region	31..55	
FT		/label= I		
FT		/note= "Transmembrane region I"		
FT		/label= II	66..91	
FT		/note= "Transmembrane region II"		
FT		/label= III	106..124	
FT		/note= "Transmembrane region III"		
FT		/note= "Ser is O-phosphorylated"	135..137	
FT		Modified-site	143..145	
FT		/note= "Ser is O-phosphorylated"		
FT		Region	150..169	
FT		/label= IV		
FT		/note= "Transmembrane region IV"		
FT		Region	192..218	
FT		/label= V		
FT		/note= "Transmembrane region V"		
FT		Region	242..266	
FT		/label= VI		
FT		/note= "Transmembrane region VI"		
FT		Region	278..298	
FT		/label= VII		
FT		/note= "Transmembrane region VII"		
XX	PX		W09803549-A1.	
XX	PO	20-JAN-1998.		
XX	XX			
XX	FX	17-JUL-1997:	G7WC-NS12536.	
XX	PP	18-JUL-1996:	G6TS-D0022185.	
XX	SX	(GSHO ) GEN HOSPITAL CORP.		
XX	PI	Reppert SM:		
XX	XX			
XX	DP	WPI: 1998-120701/11.		
XX	DR	N-PDB: V04644.		
XX	XX			
XX	PT			
XX	PT			
XX	PS	Disclosure: Page 32, 4app. English.		

This protein comprises the mouse melatonin 1a (Mel1a) receptor, a G-protein coupled receptor that specifically binds melatonin and signals the melatonin-mediated cascade of biochemical events. A claimed nucleic acid (I) comprises a functional melatonin 1a receptor gene promoter (see V04644) linked to a reporter gene. Cells containing (I) are used to screen compounds (A) for ability to alter transcription from the promoter (claimed). (A) that are activators are useful for treating circadian rhythm disorders in



FT Modified-site /note- "Extracellular domain"  
 FT 26..19 /note- "N-glycosylation site"  
 FT 23..25 /note- "N-glycosylation site"  
 FT Modified-site /note- "N-glycosylation site"  
 FT 44..68 /note- "Transmembrane region-I"  
 FT 69..79 /note- "Intracellular loop"  
 FT 78..83 /note- "Conserved melatonin receptor motif"  
 FT 80..104 /note- "Transmembrane region-II"  
 FT 105..118 /note- "Extracellular loop"  
 FT 119..137 /note- "Transmembrane region-III"  
 FT 138..162 /note- "Intracellular loop"  
 FT 145..148 /note- "Putative cytochrome-c family heme binding site"  
 FT 165..182 /note- "Transmembrane region-IV"  
 FT 183..204 /note- "Extracellular loop"  
 FT 205..231 /note- "Transmembrane region-V"  
 FT 232..254 /note- "Intracellular loop"  
 FT 255..279 /note- "Transmembrane region-VI"  
 FT 280..290 /note- "Extracellular loop"  
 FT 291..312 /note- "Transmembrane region-VII"  
 FT 307..311 /note- "Conserved melatonin receptor-1a motif"  
 FT 313..366 /note- "Intracellular domain"  
 FT Domain  
 PN WC9535320-A1.  
 XX 28-Dec-1995.  
 PD 07-JUN-1995: 95WD-HS07160.  
 PF 06-JUN-1995: 95DS-0119487.  
 PR 17-JUN-1994: 94DS-0261857.  
 PR 07-OCT-1994: 94DS-0119487.  
 XX (KASS-) MASSACHUSETTS GEN HOSPITAL.  
 PA Reprint SM:  
 PI WP1: 1996-05R368/05  
 DR N-PSDB: T09948.  
 XX  
 FT DNA encoding high affinity melatonin receptor one - used to identify  
 FT receptor agonists or antagonists e.g. for regulating circadian  
 FT rhythm disorders or reproductive cycles  
 FT  
 FT  
 PS Claim 6: Fig 2: 115pp: English.  
 CC The sequence represents a sheep high-affinity melatonin-1a  
 CC receptor, which is a membrane protein, coupled to guanine  
 CC nucleotide binding proteins (G-proteins), with 7 hydrophobic  
 CC putative transmembrane domains. Receptor fragments which interact  
 CC with melatonin or specific antagonists, may be used as  
 CC receptor-agonists or receptor-antagonists. Agonists may be used in  
 CC therapy of circadian rhythm disorders such as jet-lag or day-night  
 CC cycle disorders, to control ovulation, or in alteration of  
 CC reproductive cycles in seasonally breeding animals. Antagonists  
 CC may be used to control the initiation or timing of puberty in

CC humans. The receptor gene may also be expressed in a transgenic  
 CC animal for use as a model system to screen agonists and antagonists.  
 XX  
 SO Sequence 366 AA.  
 Query Match 54.9%, Score 1048, 181, Length 366;  
 Best Local Similarity 58.1%, Pred. No. 7,56-109;  
 Matches 205; Conservative 59; Mismatches 74; Indels 16; Gaps 5;  
 QY 4 NSPFA--NCEGCGMAVPPGMSGASAPSPPTPPVAPPAASVITVAVGVGNIV 61  
 DB 16 nssalnvsgaa-----pqad---qvppswlaatlaillftlvdivgnllv 64  
 QY 62 ILTVFNPFLPAGNLEFVSLALADLVAAFPYPIITVAIFPQWALGSEPRKASAPWA 121  
 DB 65 vlsyvrnklnmagvrvyslavadllvayppylalastvngwalslhoqslgltmg 124  
 QY 122 LSVISVENITAIINPVCYCHSMARHPTPPWITPHITCITWLTIVVAIPNPFVNST 181  
 DB 125 lsvsvstslglnatryoclochsrlgklygsnslgyltllvvaipnplvntll 184  
 QY 192 EYEPHYSTFIYIASTGVIAVWVHFLPIAVSEFLETWIVIAQPKAPESPTIC 241  
 DB 195 qyqelystfctqsvssaylavvvnflltqfmlvntvctyrlvxtlvagrvvqplvq 244  
 QY 242 LPSQLSPFLTMEVVEVVFIAICWAPLNTISLAVAINPEMAQITPDSLVISLLAVPNS 301  
 DB 245 lpsqlstfctqsvssaylavvvnflltqfmlvntvctyrlvxtlvagrvvqplvq 304  
 QY 302 CINAIVYGLNPNPPEKPKILLAIINPCHICQASKSH-ARGIQSAPPII 353  
 DB 305 cnaivylglnpnppekpkillaiinpchicqasksh-argiqsappii 353  
 RESULT 11  
 ID R88411 standard; Protein: 288 AA.  
 AC R88411;  
 XX 16-AUG-1996 (first entry)  
 DI  
 DE High-affinity melatonin-1a receptor fragment.  
 XX  
 XX Melatonin-1a receptor; human; G-protein-coupled receptor;  
 KW cytochrome-c family heme binding site; antibody;  
 KW melatonin receptor-agonist; melatonin receptor-antagonist;  
 KW circadian rhythm disorder; jet-lag; day-night cycle disorder;  
 KW ovulation; reproductive cycle; animal breeding; puberty;  
 KW Transgenic animal; drug screening.  
 XX  
 OS Homo sapiens.  
 XX  
 FU Key Location/Qualifiers  
 FT Domain 1..2  
 FT Region /note- "Intracellular loop fragment"  
 FT 1..6 /note- "Conserved melatonin receptor motif"  
 FT 3..27 /note- "Transmembrane region-II"  
 FT 28..41 /note- "Extracellular loop"  
 FT 42..60 /note- "Transmembrane region-III"  
 FT 61..85 /note- "Intracellular loop"  
 FT 86..104 /note- "Putative cytochrome-c family heme binding site"  
 FT 105..126 /note- "Extracellular loop"  
 FT Domain

FI Domain 127..153 /note- "Transmembrane region-V"  
 FI Domain 154..176 /note- "Intracellular loop"  
 FI Domain 177..201 /note- "Transmembrane region-VI"  
 FI Domain 202..212 /note- "Extracellular loop"  
 FI Domain 213..234 /note- "Transmembrane region-VII"  
 FI Region 229..233 /note- "Conserved melatonin receptor-1a motif"  
 FI Domain 235..288 /note- "Intracellular domain"  
 W09545420-A1.  
 PD 28..288 1995.  
 PF 07-JUN-1995: 95WD-US07360.  
 PR 06-JUN-1995: 95US-0319887.  
 PR 17-JUN-1994: 94US-0261857.  
 PR 07-OCT-1994: 94US-0319887.  
 PA (MASS-) MASSACHUSETTS GEN HOSPITAL.  
 PI Report SM:  
 DR WPI: 1995-058408/05.  
 DR N-PSDB: T09949.  
 XX  
 PT DNA encoding high affinity melatonin receptor one - used to identify  
 PT receptor agonists of antagonists w/4. for regulating circadian  
 PT rhythm disorders of reproductive cycles  
 PS  
 PS Claim 7: Fig 4; 115pp: English.  
 XX  
 CC The sequence represents a fragment of a human high-affinity  
 CC melatonin-1a receptor, which is a membrane protein, coupled to  
 CC guanine nucleotide binding proteins (G-proteins), with 7  
 CC hydrophobic putative transmembrane domains. The full-length  
 CC sequence is given in p88112. Receptor fragments which interact  
 CC with melatonin, or specific antagonists, may be used as  
 CC receptor-agonists or receptor-antagonists. Agonists may be used in  
 CC therapy of circadian rhythm disorders such as jetlag or day-night  
 CC cycle disorders, to control ovulation, or in alteration of  
 CC reproductive cycles in seasonally breeding animals. Antagonists  
 CC may be used to control the initiation or timing of puberty in  
 CC humans. The receptor gene may also be expressed in a transgenic  
 CC animal for use as a model system to screen agonists and antagonists.  
 XX  
 SO Sequence 288 AA:  
 Query Match: 49.9%, Score 883.5, IP 17, Length 288.  
 Host Local Similarity 50.5%, Pred. No. 2,9e-91.  
 Matches 167, Conservative 45, Mismatches 63, Indels 19, Gaps 1.

DB 150 W09545420-A1.  
 QY 415 FRREYKRLILALWNPRLHICLQASMSHAKSTQSPAP 350  
 DB 240 FRREYKRLILALWNPRLHICLQASMSHAKSTQSPAP 350  
 RESULT 12  
 ID R43913  
 AC R43913: standard; Protein: 383 AA.  
 DT 23-JUN-1994 (first entry)  
 DE Sequence of human neuro-peptide Y-peptide YY Y1 receptor.  
 EV Y1 receptor, Y1, had vasoconstriction, hypertension therapy.  
 OS Homo sapiens.  
 PN W09324515-A.  
 PD 09-DEC-1993.  
 PF 27-MAY-1993: 93WO-US05039.  
 PR 29-MAY-1992: 92US-0891453.  
 PA (CORR.) CORNELL RES FOUND INC.  
 PI Wahlestedt C:  
 DR WPI: 1993-405721/50  
 DR N-PSDB: Q52327.  
 XX  
 PT DNA encoding human neuro-peptide Y-peptide YY Y1 receptor - is  
 PT used to develop drugs for treating e.g. hypertension, depression  
 PT or obesity  
 PS  
 PS Claim 6: Page 35-36; 50pp: English.  
 XX  
 CC The lambda ZAPII cDNA library was made from mRNA of a human female  
 CC fetal (17.8 week gestation) brain using both oligo (dI) and random-  
 CC sequence primers. A 500-bp PCR product, referred to part of the  
 CC coding region (547-1047) of the rat orphan receptor was used to  
 CC screen the human fetal brain cDNA library for was performed using  
 CC the fetal brain cDNA library as template and a 23-mer forward primer  
 CC posns 547-559 (552340) and a 25-mer reverse primer posns 1023-1047  
 CC (552341). Six positive plaques were isolated and sequenced. The DNA  
 CC was amplified using two oligo primers, 381 and 382 (552342, 552343).  
 CC They correspond to the sequences juxtaposed to the linker of the pUC  
 CC plasmid and its derivative, making it possible to do PCR amplification  
 CC of a DNA cloned in the plasmid's linker. The longest clone (HY1-5)  
 CC was selected for sequencing analysis. A specific synthetic primers  
 CC (1) 5'-GATTTTTCCTG (552344-552347) and its reverse primer (552347)  
 CC were used for manual sequencing of the HY1-5 clones and its  
 CC deletion constructs. Three oligos necessary to study the inhibition  
 CC of the contractile effect of neuro-peptide Y on human blood vessels  
 CC were prepared: (1) a antisense oligo HY1 AS (corresp. to the human Y1  
 CC receptor amino terminus (552329)), (2) a sense oligo HY1-S  
 CC (552328)), and (3) a 3-base mismatched antisense oligo HY1M  
 CC (552330).  
 XX  
 SO Sequence 383 AA:  
 Query Match: 17.8%, Score 340.5, DB 14, Length 383.  
 Host Local Similarity 29.2%, Pred. No. 1e-29.  
 Matches 93, Conservative 57, Mismatches 116, Indels 43, Gaps 9.



```

43 lalagavall-----vsgnlaiaiiilvlpvtrnlllmlslllvglll 199
44 99 VALFDGALGEEHKKASAFVMSISVSNITAIINPYCYICHSMAYPIYPRW--- 155
45 98 vylmdhvfgeamcklnpfvgsllvslvllavethqllinp-----tqwrpn 150
46 156 --HTPEHICLIWLTIVALLPNFVGSLEYDPRYSCT-----FIQTAS---10 199
47 151 nhayvglavilwlvavasslp-lllygwm-depfgnltdaykkyocfdqffsdris 209
48 200 YTAAVVVIHFLPIAVSFCYLPRIWLVLAQAPKAPESPLCKPSLSPLFI-----M 253
49 200 YTAAVVVIHFLPIAVSFCYLPRIWLVLAQAPKAPESPLCKPSLSPLFI-----M 253
50 254 FVFEVIFAICWAPLNCIGLAVAINPOEMAPQIPESGLFVTSYLAVFNSCLNAVYGLNQ 313
51 265 lslvafavcwpplrlfntrfdcmhqlatcnhllilclhltamstcvrplfygdlrk 324
52 314 NFRPE 318
53 325 nfgqd 329

```

## RESULT 13

```

R35493
ID P5493 standard. Protein: 384 AA
XX
AC R35493:
XX
CT 06-SEP-1993 (first entry)
XX
TE Human NPY receptor subtype Y1.
XX

```

```

XX PCR: domain: primer: human; brain: neuropeptide Y; NPY-Y1; receptor;
XX isolation: clone: fetal; NPY; probe: adult; hippocampus; cDNA library;
XX subtype Y1; cytoplasmic loop; KC; transmembrane; G protein; rat.
XX
CS Homo sapiens.
XX
FN W09309227-A.
XX
PD 13-MAY-1993.
XX
FE 06-NOV-1992: 92W0-A000600.
XX
FR 06-NOV-1991: 91A0-0009386.
XX
FR 23-JUN-1992: 92A0-0003131.
XX
FA (GAPV-) GAPVAN INST MEDICAL RES.
XX

```

```

E1 Herzog H, Selbie L, Shine J:
XX

```

```

DE WP1: 1993-167694/20.
DE N-PSDR: Q40768.
XX

```

```

FI Human neuro-peptide Y-Y1 receptor and its DNA - useful for
FI screening for NPY agonists or antagonists
XX

```

```

FS Disclosure: Page 8-10: 32pp. English
XX

```

```

XX This sequence represents the human neuropeptide Y (NPY) receptor
XX subtype Y1. The cDNA encoding this sequence was isolated from human
XX fetal brain and human adult hippocampus cDNA libraries, using the
XX primers given in 240764-87 which correspond to positions 672-694 and
XX 48-78 in the rat cDNA clone PCR, respectively. The longest isolated
XX clone encoded the human NPY receptor subtype Y1. This clone was used
XX to probe a human genomic library which lead to the isolation of the
XX clone KC (see also R35494) which contains the NPY Y1 receptor gene.
XX The human NPY Y1 receptor consists of 3 exons and covers approx. 10
XX kb. The first 47 nucleotides of the 5' untranslated sequence of the
XX human hippocampal NPY Y1 receptor mRNA are separated by a 6 kb intron
XX from the second exon. The second intron containing an in frame stop
XX codon, is located exactly after the fifth transmembrane domain at

```

```

57 672-694-87 of the cDNA sequence. The first 47 bases of
58 the receptor is thought to form a specific domain involved in
59 determination of the specificity of coupling to different G proteins.
60
61 Sequence 384 AA:

```

```

Query Match 17.8% Score 340: DB 14: Length 384:
Post Local Similarity 29.2%: Prot No 1 20-29:
Matches 89: Conservative 57: Mismatches 117: Indels 42: Gaps 8:

```

```

CY 39 VAPLSAVLITTVAVDVGNLVLSVLPNPKLPNAGNLFVSLADIVAFPIPLIL 98
CY 43 lalagavall-----lvsqnlalililklxkmrvnlllvnlfsdlvaimcplrl 98
CY 99 VALFDGALGEEHKKASAFVMSISVSNITAIINPYCYICHSMAYPIYPRW--- 155
CY 98 vylmdhvfgeamcklnpfvgsllvslvllavethqllinp-----tqwrpn 151
CY 156 --HTPEHICLIWLTIVALLPNFVGSLEYDPRYSCT-----FIQTAS---10 199
CY 151 nhayvglavilwlvavasslp-lllygwm-depfgnltdaykkyocfdqffsdris 210
CY 200 YTAAVVVIHFLPIAVSFCYLPRIWLVLAQAPKAPESPLCKPSLSPLFI-----M 253
CY 200 YTAAVVVIHFLPIAVSFCYLPRIWLVLAQAPKAPESPLCKPSLSPLFI-----M 253
CY 254 FVFEVIFAICWAPLNCIGLAVAINPOEMAPQIPESGLFVTSYLAVFNSCLNAVYGLNQ 313
CY 265 lslvafavcwpplrlfntrfdcmhqlatcnhllilclhltamstcvrplfygdlrk 325
CY 314 NFRPE 318
CY 325 nfgqd 330

```

## RESULT 14

```

R35494
ID R35494 standard. Protein: 384 AA.
XX
AC R35494:
XX
CT 06-SEP-1993 (first entry)
XX
TE Human NPY receptor Y1.
XX

```

```

XX PCR: domain: primer: human; brain: neuropeptide Y; NPY-Y1; receptor;
XX isolation: clone: fetal; NPY; probe: adult; hippocampus; cDNA library;
XX subtype Y1; cytoplasmic loop; KC; transmembrane; G protein; rat.
XX
CS Homo sapiens.
XX
FN W09309227-A.
XX
PD 13-MAY-1993.
XX
FE 06-NOV-1992: 92W0-A000600.
XX
FR 06-NOV-1991: 91A0-0009386.
XX
FR 23-JUN-1992: 92A0-0003131.
XX
FA (GAPV-) GAPVAN INST MEDICAL RES.
XX

```

```

E1 Herzog H, Selbie L, Shine J:
XX

```

```

DE WP1: 1993-167694/20.
DE N-PSDR: Q40769.
XX

```

```

FI Human neuro-peptide Y-Y1 receptor and its DNA - useful for
FI screening for NPY agonists or antagonists
XX

```

```

FS Disclosure: Page 10-19, 32pp. English.
XX

```

XX This sequence represents the human neuropeptide Y (NPY) receptor Y1.  
 CC The DNA encoding this sequence was isolated from a human genomic  
 CC library on the clone KC. The human NPY receptor subtype Y1 cDNA (see  
 CC also R45494) was used as a probe, and was, itself, isolated from fetal  
 CC brain and human adult hippocampus cDNA libraries using the primers  
 CC 5'-GAGGCG-3' and 3'-GAGGCG-3'. The human NPY Y1 receptor  
 CC consists of 3 exons and covers approx. 10 kb. The first 57  
 CC nucleotides of the 5' untranslated sequence of the human hippocampal  
 CC NPY Y1 receptor mRNA are separated by a 6 kb intron from the second  
 CC exon. The second intron containing an in frame stop codon, is located  
 CC exactly after the fifth transmembrane domain at nucleotide 408 of the  
 CC cDNA sequence. The third cytoplasmic loop of the receptor is thought  
 CC to form a specific domain involved in determination of the specificity  
 CC of coupling to different G proteins.

XX Sequence 384 AA:

Query Match 17.8% Score 340: DB 14: Length 384:  
 Best Local Similarity 29.2%: Pred. No. 1,20-29:  
 Matches 89: Conservative 57: Mismatches 117: Indels 41: Gaps 8:

UY 39 VAPALSAVITAVDVNLTIVTSVLPKIPNAGNLFVSLADLVAVPYPLD 98  
 DB 43 IALAYGAVII-----IYSGNIALIIIIKQKEMRVNIIIVLSFSLVAMCIPITF 98  
 UY 99 VAIFFVGMALGEPRKASAFVWGLSVGSVENITAIINPYCYICHSMAYHRYPRM--- 155  
 DB 99 VYIIMHWKFGAEMCKINPVGCVSITVSLFSLVLAVERHQLINP-----YQWRPN 151  
 UY 156 --HTPLHICILMLLVALLPNFVGSLEYDPRIVSCT-----FIQTAS-----TQ 199  
 DB 152 NTHAYGVIAVIAWLAASSIP-FLIYGMDEPFQVTLIDAYKDYKVCIDQIPSDSHLS 210  
 UY 200 YTAAVVVIHFLPIAVVSPCYLPRIWLVDAAPKAPESRILCKPSDLSFUT-----M 253  
 DB 211 YTIILIVGYFPICTFICICGYKLY-----FLKRNMMKMDKYSSEKKEINML 265  
 UY 254 VAVFVFAICAPLNCIGLAVAINPQMAQIPESLFTVSYLLAFNSLNAVYGLNQ 313  
 DB 266 IATVAVIACVCFITIGVIGWCHHILATCCHNIIILCHLAAIATSTCVPIFYFLNK 325  
 UY 414 NKKRPE 318  
 DB 426 ATGAG 339

RESUME 15

W01014 standard: protein: 398 AA.

AC W01014:

XX 12-FEB-1997 (first entry)

DE Modified neuropeptide Y receptor (deletion mutant).

KM Neuropeptide Y receptor, NPY, modified mutant, adenylate cyclase,

KM predicted modified receptor, beta-adrenergic receptor, agonist,

KM antagonist, suppressor, inducer, screening, identification,

KM treatment, obesity, diabetes, anxiety, hypertension,

KM congestive heart failure, cardiac and cerebral vasospasm,

KM pheochromocytoma, ganglioglioma, Huntington's disease,

KM Alzheimer's disease, Parkinson's disease.

XX Homo sapiens:

XX Misc-difference 398

XX Location/Qualifiers

XX Note="Unidentified amino acid."

XX 17-MAY-1996.  
 XX UP-NIV-1995: 95WU-US14377.  
 XX 07-NIV-1994: 94US-0445017  
 XX (MFRP) MFRP & CO INC.  
 XX Casolari MA, Macneil DJ, Strader CD:  
 XX NPY, 1996-101551/32.  
 XX Neuro-peptide Y receptor modified in third intracellular domain  
 XX useful to identify modulators of receptor activity for treating e.g.  
 XX obesity, diabetes, hypertension, congestive heart failure, etc.  
 XX Disclosure: Page 28: 59pp: English.

CC Certain mutations in the third intracellular domain of the G-coupled  
 CC beta-adrenergic neuropeptide Y (NPY) receptor lead to loss of  
 CC functional, adenylyl cyclase activation via a protein binding  
 CC interference. Similar alterations in the NPY receptor may also lead  
 CC to 5-protein interference and modified 2nd messenger responses. The  
 CC modified NPY receptor can be used to identify compounds that  
 CC modulate modified NPY receptor activity. These, then identified,  
 CC agonists, antagonists, suppressors and inducers can then be used to  
 CC treat obesity, diabetes, anxiety, hypertension, congestive heart  
 CC failure, cardiac and cerebral vasospasm, pheochromocytoma and  
 CC ganglioglioma, as well as Huntington's, Alzheimer's and  
 CC Parkinson's diseases. This deletion mutant had a 13 residue  
 CC sequence removed which preceded the Arg residue formerly at  
 CC position 266 (see W03014 for the wild type sequence).

XX Sequence 398 AA:

Query Match 17.8% Score 310: DB 17: Length 398:  
 Best Local Similarity 28.9%: Pred. No. 1,60-29:  
 Matches 90: Conservative 57: Mismatches 120: Indels 44: Gaps 8:

UY 39 VAPALSAVITAVDVNLTIVTSVLPKIPNAGNLFVSLADLVAVPYPLD 98  
 DB 46 IALAYGAVII-----IYSGNIALIIIIKQKEMRVNIIIVLSFSLVAMCIPITF 101  
 UY 99 VAIFFVGMALGEPRKASAFVWGLSVGSVENITAIINPYCYICHSMAYHRYPRM--- 155  
 DB 102 YTIIMHWKFGAEMCKINPVGCVSITVSLFSLVLAVERHQLINP-----YQWRPN 154  
 UY 156 --HTPLHICILMLLVALLPNFVGSLEYDPRIVSCT-----FIQTAS-----TQ 199  
 DB 155 NTHAYGVIAVIAWLAASSIP-FLIYGMDEPFQVTLIDAYKDYKVCIDQIPSDSHLS 214  
 UY 200 YTAAVVVIHFLPIAVVSPCYLPRIWLVDAAPKAPESRILCKPSDLSFUT-----M 247  
 DB 214 YTIILIVGYFPICTFICICGYKLY-----FLKRNMMKMDKYSSEKKEINML 267  
 UY 248 VAVFVFAICAPLNCIGLAVAINPQMAQIPESLFTVSYLLAFNSLNAVYGLNQ 307  
 DB 272 YTIIMHWKFGAEMCKINPVGCVSITVSLFSLVLAVERHQLINP-----YQWRPN 322  
 UY 308 YGLINQKPRPE 318  
 DB 333 YGLINQKPRPE 343

Search completed: February 18, 2001, 20:18:12  
 Job time: 12784 sec

Genome version 4.5  
Copyright (c) 1999 - 2000 - Empress Ltd

OW protein - protein search using sw model

Run on: February 19, 2001 16:49:54 : Search time 54.19 seconds  
(without alignments)  
119,979 Million cell updates/sec

Title: US-09-226-046-16

Perfect score: 1 MSENOSFANCTEASAKAVP

ENLSTAFETLTVNLSALML 302

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 174772 seqs, 17957048 residues

Total number of hits satisfying chosen parameters: 174772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA\*

1: US0466103A-16  
2: US0466103A-16  
3: US0466103A-16  
4: US0466103A-16  
5: US0466103A-16

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	1908	100.0	362	US-08-466-103A-16	Sequence 1, Appl
2	1123	59.9	428	US-08-466-103A-16	Sequence 1, Appl
3	1088	57.0	350	US-09-466-103A-12	Sequence 12, Appl
4	1086.5	56.5	353	US-08-466-103A-16	Sequence 1, Appl
5	1072.5	56.2	353	US-09-466-103A-12	Sequence 12, Appl
6	1066.5	55.9	353	US-08-466-103A-16	Sequence 1, Appl
7	1048	54.9	366	US-08-466-103A-16	Sequence 1, Appl
8	1048	54.9	366	US-08-466-103A-16	Sequence 1, Appl
9	849.5	45.9	405	US-08-466-103A-16	Sequence 1, Appl
10	835	43.8	257	US-08-466-103A-16	Sequence 1, Appl
11	511	26.8	153	US-08-466-103A-16	Sequence 1, Appl
12	340	17.8	383	US-09-466-103A-12	Sequence 12, Appl
13	340	17.8	383	US-08-466-103A-16	Sequence 1, Appl
14	340	17.8	383	US-08-466-103A-16	Sequence 1, Appl
15	340	17.8	383	US-08-466-103A-16	Sequence 1, Appl
16	337.5	17.7	411	US-08-466-103A-16	Sequence 1, Appl
17	337.5	17.7	411	US-08-466-103A-16	Sequence 1, Appl
18	337	17.7	392	US-09-466-103A-12	Sequence 12, Appl
19	337	17.7	392	US-08-466-103A-16	Sequence 1, Appl
20	337	17.7	392	US-08-466-103A-16	Sequence 1, Appl
21	337	17.7	392	US-08-466-103A-16	Sequence 1, Appl
22	329.5	17.3	382	US-08-466-103A-16	Sequence 1, Appl
23	329.5	17.3	382	US-08-466-103A-16	Sequence 1, Appl
24	329.5	17.3	382	US-08-466-103A-16	Sequence 1, Appl
25	329.5	17.3	382	US-08-466-103A-16	Sequence 1, Appl
26	329.5	17.3	382	US-08-466-103A-16	Sequence 1, Appl
27	324	17.0	391	US-08-466-103A-16	Sequence 1, Appl
28	321	16.5	409	US-08-466-103A-16	Sequence 1, Appl

29	321	16.8	370	US-09-512-974B-323	Sequence 23, Appl
30	318.5	16.7	391	US-07-816-243-4	Sequence 2, Appl
31	318.5	16.7	391	US-07-816-243-4	Sequence 2, Appl
32	318.5	16.7	391	US-08-417-103-14	Sequence 14, Appl
33	314.5	16.5	391	US-07-816-283-4	Sequence 4, Appl
34	314.5	16.5	391	US-08-417-103-4	Sequence 4, Appl
35	312	16.4	375	US-08-126-412-2	Sequence 2, Appl
36	312	16.4	375	US-08-555-268A-13	Sequence 2, Appl
37	312	16.4	375	US-08-495-695B-2	Sequence 2, Appl
38	312	16.4	375	US-08-495-695B-2	Sequence 2, Appl
39	311	16.3	350	US-08-495-695B-2	Sequence 3, Appl
40	310.5	16.3	369	US-07-816-283-8	Sequence 8, Appl
41	310.5	16.3	369	US-08-417-103-8	Sequence 8, Appl
42	308	16.1	513	US-08-411-854-3	Sequence 8, Appl
43	308	16.1	513	US-08-406-855A-21	Sequence 21, Appl
44	308	16.1	513	US-09-206-899-21	Sequence 21, Appl
45	308	16.1	515	US-08-444-714A-7	Sequence 7, Appl

## ALIGNMENTS

RESULT 1  
US-08-466-103A-16  
Sequence 16, Application US/08466103A  
Patent No. 5856124  
GENERAL INFORMATION:  
APPLICANT: Reppert, Steven M.  
APPLICANT: Edisawa, Takashi  
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
TITLE OF INVENTION: PEPTIDES AND USES THEREOF  
NUMBER OF INVENTION: 29  
REFERENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08466103A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/219,897  
FILING DATE: 07-OCT-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/261,857  
FILING DATE: 17-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Fraser, Jais K.  
PREPARATION NUMBER: 34,819  
REFERENCE/EXETER NUMBER: 17262560002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-8906  
FAX: 617/542-8906  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 362 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
FRAGMENT TYPE: Internal  
US-08-466-103A-16  
Query Match: 100.0%, Score 1908, EE 0, Length 362  
Best Local Similarity: 100.0%, Score 1908, EE 0, Length 362

Matches 462: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSFNSFANCCFAGCAVAPPCWAGAGAPSPPTPPPPVAPALSAVIVITAVVGNIT 60  
 D 1 MSFNSFANCCFAGCAVAPPCWAGAGAPSPPTPPPPVAPALSAVIVITAVVGNIT 60

QY 61 VILSVLNRRKLRNAGNCLVLSLADLVAFYPPYLIVAFYDGMALGEHCASAFVM 120  
 D 61 VILSVLNRRKLRNAGNCLVLSLADLVAFYPPYLIVAFYDGMALGEHCASAFVM 120

QY 121 GLSVGSVENITAIINRCYICHSMAVHRIPRMTPLHICLILTVALLPNFVGS 180  
 D 121 GLSVGSVENITAIINRCYICHSMAVHRIPRMTPLHICLILTVALLPNFVGS 180

QY 141 LEYDPRIVSTCTGTASTGYTAAVVTHFLPLIAVVSFCYLPWVIQAPKAPPSRL 240  
 D 141 LEYDPRIVSTCTGTASTGYTAAVVTHFLPLIAVVSFCYLPWVIQAPKAPPSRL 240

QY 241 CLKRSRLSELTTRVVVYFAICAPLNCIGLAVAINPQMAQOIEGLFVTSYLLAYN 300  
 D 241 CLKRSRLSELTTRVVVYFAICAPLNCIGLAVAINPQMAQOIEGLFVTSYLLAYN 300

QY 401 SCNAIVVGLINQNPPEKFKILLALNPHHCIDASKSGSHAGLSAPPIIGVGHAD 360  
 D 401 SCNAIVVGLINQNPPEKFKILLALNPHHCIDASKSGSHAGLSAPPIIGVGHAD 360

QY 661 AL 362  
 D 661 AL 362

RESULT 2  
 Sequence 2, Application US/09466103A  
 Patent No. 5856124  
 GENERAL INFORMATION:  
 APPLICANT: Reppert, Steven M.  
 APPLICANT: Edisawa, Takashi  
 TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
 TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 275 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: US  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows95  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/466,103A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/319,887  
 FILING DATE: 07-OCT-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/261,867  
 FILING DATE: 17-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Janis K.  
 REGISTRATION NUMBER: 34,819  
 TELEPHONE: 617/642-5070  
 TELEFAX: 617/642-5070  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 420 amino acids

TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-09-466-103A-2

Query Match 58.9%; Score 1123; DB 2; Length 420;  
 Best Local Similarity 59.4%; Freq. No. 3,147,85;  
 Matches 215: Conservative 59; Mismatches 78; Indels 10; Gaps 3;

QY 1 MSFNSFANCCFAGCAVAPPCWAGAGAPSPPTPPPPVAPALSAVIVITAVVGNIT 60  
 D 2 MSFNSFANCCFAGCAVAPPCWAGAGAPSPPTPPPPVAPALSAVIVITAVVGNIT 60

QY 61 VILSVLNRRKLRNAGNCLVLSLADLVAFYPPYLIVAFYDGMALGEHCASAFVM 120  
 D 53 VILSVLNRRKLRNAGNCLVLSLADLVAFYPPYLIVAFYDGMALGEHCASAFVM 112

QY 121 GLSVGSVENITAIINRCYICHSMAVHRIPRMTPLHICLILTVALLPNFVGS 180  
 D 113 GLSVGSVENITAIINRCYICHSMAVHRIPRMTPLHICLILTVALLPNFVGS 172

QY 141 LEYDPRIVSTCTGTASTGYTAAVVTHFLPLIAVVSFCYLPWVIQAPKAPPSRL 240  
 D 173 LEYDPRIVSTCTGTASTGYTAAVVTHFLPLIAVVSFCYLPWVIQAPKAPPSRL 232

QY 241 CLKRSRLSELTTRVVVYFAICAPLNCIGLAVAINPQMAQOIEGLFVTSYLLAYN 300  
 D 233 CLKRSRLSELTTRVVVYFAICAPLNCIGLAVAINPQMAQOIEGLFVTSYLLAYN 292

QY 401 SCNAIVVGLINQNPPEKFKILLALNPHHCIDASKSGSHAGLSAPPIIGVGHAD 360  
 D 361 AL 362

QY 361 AL 362  
 D 352 ML 353

RESULT 3  
 Sequence 12, Application US/09466103A  
 Patent No. 5856124  
 GENERAL INFORMATION:  
 APPLICANT: Reppert, Steven M.  
 APPLICANT: Edisawa, Takashi  
 TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
 TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson P.C.  
 STREET: 275 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: US  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: Windows95  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 08/319,887  
 FILING DATE: 07-OCT-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Janis K.  
 REGISTRATION NUMBER: 34,819  
 TELEPHONE: 617/642-5070  
 TELEFAX: 617/642-5070  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 420 amino acids

NAME: Fraser, Janis K  
 REGISTRATION NUMBER: 34,819  
 REFERENCE/DECKET NUMBER: 00780/450002  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5070  
 TELEFAX: 617/542-8006  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 350 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FRAGMENT TYPE: internal  
 US-08-406-103A-12

Query Match 57.04: Score 1088; DB 2; Length 350;  
 Best Local Similarity 61.28; Pred. No. 1,9e+82;  
 Matches 205; Conservative 52; Mismatches 70; Indels 8; Gaps 1;

24 GAGSAPRSPT-----PRPWAPALSAVLIVIAVWVSNLIVLSYLNKLNAG 75  
 3 GNSGALPAPASQPLRGSGAPPSWIASALCVLFTIVDLSNLIVLSYLNKLNAG 62  
 76 NLFVSLADLVVAFYPIPLIYAIYDGMAGEHCKASAFVGLSVISVFNTAIA 135  
 63 NIFVSLADLVVAFYPIPLIYAIYDGMAGEHCKASAFVGLSVISVFNTAIA 122  
 136 INPVCYCHSAVRYRYRMTPLHGLIMLVNVALIPFVPSLEYDPRVYSCPT 195  
 123 INPVCYCHSKYKYLKSSKNSICVYIIMVITIAVILPMLPGTGLQYDPTYSCTPAQS 182  
 146 ASCTYAAVVVHLEPLIAVVSFYRTWIVIGAPFAPRSPTIKPSPTFTMEV 257  
 143 VSAATIAVVVHLEPLIIVICVILKIMLVIGVGVKPKPKIKGPHFNFTMEV 242  
 256 VFVFAITMAVNLNIGLVAINDGMAPVYFESLIVSLAIFNSLNAVSLNAN 312  
 243 VFVFAITMAVNLNIGLVAINDGMAPVYFESLIVSLAIFNSLNAVSLNAN 302  
 316 PRFPRPITIAIWNPHCTIQDASKGSHAEIUSFAP 350  
 303 RKFYPRITVSTAPVFEVSSNVAVRVMKRSF 337

RESULT 4  
 US-08-896-465-6  
 Sequence 6, Application US/08896365  
 Patent No. 5939264  
 GENERAL INFORMATION:  
 APPLICANT: Polischild, Max F.  
 APPLICANT: Tugde, Christopher K.  
 APPLICANT: Messer, Lori A.  
 APPLICANT: Tun-Ping, Yu  
 TITLE OF INVENTION: GENES AND GENETIC MARKERS FOR IMPROVED  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Farley, McKee, Thomas, Woodhous & Sasse  
 STREET: 801 Grand Avenue, Suite 3000  
 CITY: Des Moines  
 STATE: Iowa  
 COUNTRY: USA  
 ZIP: 50309

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0 Version #1.10  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/896,365  
 FILING DATE: 18-JUL-1997  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/022,180  
 FILING DATE: 18-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Nebel, Heidi S.  
 REGISTRATION NUMBER: 37,719  
 REFERENCE/DECKET NUMBER: 18MP 021591  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 515-288-3667  
 TELEFAX: 515-288-1338  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 353 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: unknown  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 CELL TYPE: Melanocyte  
 CELL LINE: human melanin receptor 1a  
 POSITION IN GENOME:  
 MAP POSITION: 14  
 US-08-896-365-6

Query Match 56.94: Score 1086; DB 2; Length 353;  
 Best Local Similarity 60.74; Pred. No. 4.6e+82;  
 Matches 205; Conservative 52; Mismatches 70; Indels 11; Gaps 1;

24 GAGSAPRSPT-----PRPWAPALSAVLIVIAVWVSNLIVLSYLNKLNAG 72  
 3 GNSGALPAPASQPLRGSGAPPSWIASALCVLFTIVDLSNLIVLSYLNKLNAG 62  
 73 NNSGLFVSAATIAVVVHLEPLIIVICVILKIMLVIGVGVKPKPKIKGPHFNFTMEV 132  
 63 NNSGIFVSAATIAVVVHLEPLIIVICVILKIMLVIGVGVKPKPKIKGPHFNFTMEV 122  
 133 AIANPVCYCHSAVRYRYRMTPLHGLIMLVNVALIPFVPSLEYDPRVYSCPT 192  
 123 AIANPVCYCHSKYKYLKSSKNSICVYIIMVITIAVILPMLPGTGLQYDPTYSCTPAQS 182  
 193 IQVASTGYIAAVVHLEPLIAVVSQYLIWLVIGAPFAPRSPTIKPSPTFTMEV 252  
 183 IQVASTGYIAAVVHLEPLIIVICVILKIMLVIGVGVKPKPKIKGPHFNFTMEV 242  
 253 MFVFAITMAVNLNIGLVAINDGMAPVYFESLIVSLAIFNSLNAVSLNAN 312  
 243 MFVFAITMAVNLNIGLVAINDGMAPVYFESLIVSLAIFNSLNAVSLNAN 302  
 313 GNPFRPITIAIWNPHCTIQDASKGSHAEIUSFAP 350  
 303 GNPFRPITVSTAPVFEVSSNVAVRVMKRSF 340

RESULT 5  
 US-09-280-420-2  
 Sequence 2, Application US/09280420  
 Patent No. 6037131  
 GENERAL INFORMATION:  
 APPLICANT: Reppert, Steven M.  
 TITLE OF INVENTION: MELATONIN 1A RECEPTOR GENE  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson, P.C.  
 STREET: 325 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: US  
 ZIP: 02110-2804

## \*\*\*\*\* MEDIUM READABLE FORM \*\*\*\*\*

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/250,420

## \*\*\*\*\* FILING DATE \*\*\*\*\*

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/895,701

## \*\*\*\*\* FILING DATE \*\*\*\*\*

APPLICATION NUMBER: 08/022,185  
FILING DATE: 18-JUL-1996

## \*\*\*\*\* ATTORNEY/AGENT INFORMATION \*\*\*\*\*

NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/EXCEL NUMBER: 00786/340002

## \*\*\*\*\* TELEPHONE/TELEFAX \*\*\*\*\*

TELEPHONE: 617/542-5070  
TELEFAX: 617/542-5070

## \*\*\*\*\* INFORMATION FOR SEQ ID NO: 2 \*\*\*\*\*

SEQUENCE CHARACTERISTICS:  
LENGTH: 353 amino acids  
TYPE: amino acid

## \*\*\*\*\* MOLECULE TYPE \*\*\*\*\*

MOLECULE TYPE: Protein  
FRAGMENT TYPE: Internal

## \*\*\*\*\* US-09 \*\*\*\*\*

US-09 280,420-2

## \*\*\*\*\* Query Match \*\*\*\*\*

Best Local Similarity 56.28; Score 1072.5; DB 3; Length 353;  
Matches 199; Conservative 58; Mismatches 70; Indels 7; Gaps 2;

```

20 PMSGASGASRPSPRPVAVAPALSAVLTAVVAVVGNLVLTLVLEPKLPNAGNLEL 79
DB 16 PMSGASGASRPSPRPVAVAPALSAVLTAVVAVVGNLVLTLVLEPKLPNAGNLEL 79
20 PMSGASGASRPSPRPVAVAPALSAVLTAVVAVVGNLVLTLVLEPKLPNAGNLEL 79
DB 16 PMSGASGASRPSPRPVAVAPALSAVLTAVVAVVGNLVLTLVLEPKLPNAGNLEL 79
80 VSLAALAVVAVVPPPLVIAVIFGQWALGFRHCKASAFWGLSVGSVNTAIAINPY 139
DB 70 VSLAALAVVAVVPPPLVIAVIFGQWALGFRHCKASAFWGLSVGSVNTAIAINPY 139
140 CYCHSMAYHRIYRPMHTPLHICLIMLIVALLPNFVGSLEVDPRISCTFIQTASTQ 199
DB 140 CYCHSMAYHRIYRPMHTPLHICLIMLIVALLPNFVGSLEVDPRISCTFIQTASTQ 199
200 YTAANVAVHFLPLIAVVSFCYLRIVWLVLQAPRKAPKPSPLCLKPSDLPSFLIMEVAVI 259
DB 200 YTAANVAVHFLPLIAVVSFCYLRIVWLVLQAPRKAPKPSPLCLKPSDLPSFLIMEVAVI 259
260 FAICWAPLNTIGLAVAINQEMAPQIEGELVSYLLAVFNSCLNAIVYGLINQNPFRFY 319
DB 260 FAICWAPLNTIGLAVAINQEMAPQIEGELVSYLLAVFNSCLNAIVYGLINQNPFRFY 319
320 KRLLALMNPRIHODASKGSHAGDLSAPAPPI 353
DB 320 KRLLALMNPRIHODASKGSHAGDLSAPAPPI 353

```

## \*\*\*\*\* RESULT \*\*\*\*\*

US-08-466-103A-14  
Sequence 14, Application US/08466103A  
Patent No. 5856124

## \*\*\*\*\* GENERAL INFORMATION \*\*\*\*\*

APPLICANT: Ropert, Steven M.  
APPLICANT: Edisawa, Takashi

TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
RECEPTORS AND USES THEREOF

NUMBER OF SEQUENCES: 29  
ADDRESS/AGENT ADDRESS:  
ADDRESS: Fish & Richardson P.C.

STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804

## \*\*\*\*\* MEDIUM READABLE FORM \*\*\*\*\*

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/466,103A

## \*\*\*\*\* FILING DATE \*\*\*\*\*

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/319,887

## \*\*\*\*\* FILING DATE \*\*\*\*\*

APPLICATION NUMBER: 08/022,185  
FILING DATE: 17-JUN-1994

## \*\*\*\*\* ATTORNEY/AGENT INFORMATION \*\*\*\*\*

NAME: Fraser, Janis K.  
REGISTRATION NUMBER: 34,819  
REFERENCE/EXCEL NUMBER: 00786/340002

## \*\*\*\*\* TELEPHONE/TELEFAX \*\*\*\*\*

TELEPHONE: 617/542-5070  
TELEFAX: 617/542-5070

## \*\*\*\*\* INFORMATION FOR SEQ ID NO: 14 \*\*\*\*\*

SEQUENCE CHARACTERISTICS:  
LENGTH: 353 amino acids  
TYPE: amino acid

## \*\*\*\*\* MOLECULE TYPE \*\*\*\*\*

MOLECULE TYPE: Protein  
FRAGMENT TYPE: Internal

## \*\*\*\*\* US-08 \*\*\*\*\*

US-08-466-103A-14

## \*\*\*\*\* Query Match \*\*\*\*\*

Best Local Similarity 55.94; Score 1065.5; DB 2; Length 353;  
Matches 198; Conservative 58; Mismatches 71; Indels 7; Gaps 2;

```

20 PMSGASGASRPSPRPVAVAPALSAVLTAVVAVVGNLVLTLVLEPKLPNAGNLEL 79
DB 16 PMSGASGASRPSPRPVAVAPALSAVLTAVVAVVGNLVLTLVLEPKLPNAGNLEL 79
20 PMSGASGASRPSPRPVAVAPALSAVLTAVVAVVGNLVLTLVLEPKLPNAGNLEL 79
DB 16 PMSGASGASRPSPRPVAVAPALSAVLTAVVAVVGNLVLTLVLEPKLPNAGNLEL 79
80 VSLAALAVVAVVPPPLVIAVIFGQWALGFRHCKASAFWGLSVGSVNTAIAINPY 139
DB 70 VSLAALAVVAVVPPPLVIAVIFGQWALGFRHCKASAFWGLSVGSVNTAIAINPY 139
140 CYCHSMAYHRIYRPMHTPLHICLIMLIVALLPNFVGSLEVDPRISCTFIQTASTQ 199
DB 140 CYCHSMAYHRIYRPMHTPLHICLIMLIVALLPNFVGSLEVDPRISCTFIQTASTQ 199
200 YTAANVAVHFLPLIAVVSFCYLRIVWLVLQAPRKAPKPSPLCLKPSDLPSFLIMEVAVI 259
DB 200 YTAANVAVHFLPLIAVVSFCYLRIVWLVLQAPRKAPKPSPLCLKPSDLPSFLIMEVAVI 259
260 FAICWAPLNTIGLAVAINQEMAPQIEGELVSYLLAVFNSCLNAIVYGLINQNPFRFY 319
DB 260 FAICWAPLNTIGLAVAINQEMAPQIEGELVSYLLAVFNSCLNAIVYGLINQNPFRFY 319
320 KRLLALMNPRIHODASKGSHAGDLSAPAPPI 353
DB 320 KRLLALMNPRIHODASKGSHAGDLSAPAPPI 353

```

## \*\*\*\*\* RESULT \*\*\*\*\*

US-08-466-103A-4  
Sequence 4, Application US/08466103A  
Patent No. 5856124

## \*\*\*\*\* GENERAL INFORMATION \*\*\*\*\*

APPLICANT: Ropert, Steven M.  
APPLICANT: Edisawa, Takashi

TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
RECEPTORS AND USES THEREOF

NUMBER OF SEQUENCES: 29  
ADDRESS/AGENT ADDRESS:  
ADDRESS: Fish & Richardson P.C.

```

1 TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
2 TITLE OF INVENTION: RECEPTORS AND USFS THEREOF
3 NUMBER OF SEQUENCES: 29
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: Fish & Richardson P.C.
6 STREET: 225 Franklin Street
7 CITY: Boston
8 STATE: MA
9 COUNTRY: US
10 ZIP: 02110-2804
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Diskette
13 COMPUTER: IBM Compatible
14 OPERATING SYSTEM: Windows95
15 SOFTWARE: FastSeq for Windows Version 2.0
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US-08/466,103A
18 FILING DATE: 06-JUN-1995
19 CLASSIFICATION: 435
20 PRIORITY APPLICATION DATA:
21 APPLICATION NUMBER: 08/319,587
22 FILING DATE: 07-OCT-1994
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 08/261,857
25 FILING DATE: 17-JUN-1994
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Frazer, Janis K.
28 REGISTRATION NUMBER: 34,819
29 REFERENCE/DOCKET NUMBER: 00796/250002
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 617/542-5070
32 TELEFAX: 617/542-8966
33 INFORMATION FOR SEQ ID NO: 4:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 366 amino acids
36 TYPE: amino acid
37 TOPOLOGY: linear
38 MOLECULE TYPE: Protein
39 FRAGMENT TYPE: Internal
40 US-08-466-103A-4

Query Match 54 9% Score 1048; DR 2; Length 366;
Best Local Similarity 58.1%; Pred. No. 46-79;
Matches 205; Conservative 58; Mismatches 74; Indels 16; Gaps 5;

C 4 NCSEA--NCCFAGSMAVFRGWSGASAPFRSRTPPPWAPALSAVILVITAVVGNLLV 61
D 15 NSSALLNWSQAA-----PGADP---GVPPFSWLAATLASILIFTIVDIVGNLLV 64
Q 62 ILTVLBNKLNAGNLFIVSLADLVAFYPPYLILVAIFYGMAIGEHCASAFVNC 121
D 65 VLSVBNKLNAGNLFIVSLADLVAFYPPYLILVAIFYGMAIGEHCASAFVNC 124
Q 122 LSVIGSVFNITAINPYCYICHSMAYHPYPMHTPLHLILMLITVAIPVFGSL 181
D 125 LSVIGSVFNITAINPYCYICHSMAYHPYPMHTPLHLILMLITVAIPVFGSL 184
Q 182 FYDPRIYSCIFIGASTGYTAAVVVHFLIPAVSPCYERIMVLYIGAPKAPPSRLC 241
D 185 QYDPRIYSCIFIGASTGYTAAVVVHFLIPAVSPCYERIMVLYIGAPKAPPSRLC 244
Q 242 LKPSDLPSFLTFMVFVFAITWAMNLTAVAINLEMAPDIPESJFVSTLAHNS 301
D 245 LKPSDLPSFLTFMVFVFAITWAMNLTAVAINLEMAPDIPESJFVSTLAHNS 304
Q 302 CINAIVGLLNCNFRREKRIILALMNRHDIQASKGSH-AESIQSAPRTI 353
D 305 CINAIVGLLNCNFRREKRIILALMNRHDIQASKGSH-AESIQSAPRTI 355

```

```

1 Sequence 7: Application US/08896365
2 Patent No. 5939264
3 GENERAL INFORMATION:
4 APPLICANT: Rothschild, Max F.
5 APPLICANT: Tugale, Christopher K.
6 APPLICANT: Messer, Lori A.
7 APPLICANT: Tun-Ping, Yu
8 TITLE OF INVENTION: GENES AND GENETIC MARKERS FOR IMPROVED
9 NUMBER OF SEQUENCES: 25
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
12 STREET: 801 Grand Avenue, Suite 3200
13 CITY: Des Moines
14 STATE: Iowa
15 COUNTRY: USA
16 ZIP: 50309
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: Patentia Release #1.0, Version #1.30
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/896,365
24 FILING DATE: 18-JUL-1997
25 CLASSIFICATION: 435
26 PRIORITY APPLICATION DATA:
27 APPLICATION NUMBER: US 59/042,180
28 FILING DATE: 19-JUL-1995
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Nebel, Heidi S.
31 REGISTRATION NUMBER: 37,719
32 REFERENCE/DOCKET NUMBER: 199P 221591
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 515-288-3667
35 TELEFAX: 515-288-1338
36 INFORMATION FOR SEQ ID NO: 7:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 366 amino acids
39 TYPE: amino acid
40 STRANDEDNESS: single
41 TOPOLOGY: unknown
42 MOLECULE TYPE: cDNA
43 HYPOTHETICAL: NO
44 ANTI-SENSE: NO
45 ORIGINAL SOURCE:
46 ORGANISM: Ovis ammon aries
47 CELL TYPE: Melanocyte
48 US-08-896-365-7

Query Match 54 9% Score 1048; DR 2; Length 366;
Best Local Similarity 58.1%; Pred. No. 46-79;
Matches 205; Conservative 58; Mismatches 74; Indels 16; Gaps 5;

D 16 NSSALLNWSQAA-----PGADP---GVPPFSWLAATLASILIFTIVDIVGNLLV 64
Q 62 ILTVLBNKLNAGNLFIVSLADLVAFYPPYLILVAIFYGMAIGEHCASAFVNC 121
D 65 VLSVBNKLNAGNLFIVSLADLVAFYPPYLILVAIFYGMAIGEHCASAFVNC 124
Q 122 LSVIGSVFNITAINPYCYICHSMAYHPYPMHTPLHLILMLITVAIPVFGSL 181
D 125 LSVIGSVFNITAINPYCYICHSMAYHPYPMHTPLHLILMLITVAIPVFGSL 184
Q 182 FYDPRIYSCIFIGASTGYTAAVVVHFLIPAVSPCYERIMVLYIGAPKAPPSRLC 241
D 185 QYDPRIYSCIFIGASTGYTAAVVVHFLIPAVSPCYERIMVLYIGAPKAPPSRLC 244
Q 242 LKPSDLPSFLTFMVFVFAITWAMNLTAVAINLEMAPDIPESJFVSTLAHNS 301
D 245 LKPSDLPSFLTFMVFVFAITWAMNLTAVAINLEMAPDIPESJFVSTLAHNS 304

```

DB 245 LKNGPBNVTMEVYVLEFAICWAPI NIGLVASDPASAPRIPEWLEVASVYMAVENS 304

0Y 402 GINAIYVGLNPNFRERERKILLALMNPRLIQLASKOSH AEDUQSAAPP11 353  
 DB 406 GINAIYVGLNPNFRERERKILLALMNPRLIQLASKOSH AEDUQSAAPP11 355

RESULT: 9

US-08-466-10YA-6  
 Sequence 6, Application US/08466103A  
 Patent No. 5852124

# GENERAL INFORMATION:

APPLICANT: Poppey, Steven M.  
 APPLICANT: Edisawa, Takashi  
 TITLE OF INVENTION: HIGH-AFFINITY MELATONIN  
 TITLE OF INVENTION: RECEPTORS AND USES THEREOF  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Fish & Richardson P C  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: MA  
 COUNTRY: US  
 ZIP: 02110-2804

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 OPERATING SYSTEM: Windows95

SOURCEWARE: FastSeq for Windows Version 4.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08466103A  
 FILING DATE: 06-JUN-1995

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/419,887  
 FILING DATE: 07-OCT-1994

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/251,857  
 FILING DATE: 17-JUN-1994

ATTORNEY/AGENT INFORMATION:  
 NAME: Fraser, Jais K.  
 REGISTRATION NUMBER: 34,819  
 REFERENCE/AGENT NUMBER: 00794/2560002

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 617/542-5879  
 TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 288 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear

MOLECULE TYPE: Protein  
 FRAGMENT TYPE: Internal  
 US-08-466-10YA-6

Query Match 46.8%; Score 889.5; DB 2; Length 288;  
 Best Local Similarity 60.5%; Pred. No. 3.5e-65;  
 Matches 157; Substitutive 45; Mismatches 53; Indels 1; Gaps 1;

0Y 75 GNFELVSLANAT VAAVYPPYI IIAVIFDQALGEGHCKASAFVMSI SVIGSVFNITAI 134

DB 1 GNFELVSLANAT VAAVYPPYI IIAVIFDQALGEGHCKASAFVMSI SVIGSVFNITAI 134

0Y 61 AINRYCYIHSK KOKYVSSKSGIVVIT IAVIPNIPROGLQYEPRIISCTFAQ 119

DB 61 AINRYCYIHSK KOKYVSSKSGIVVIT IAVIPNIPROGLQYEPRIISCTFAQ 119

0Y 195 IASTGYTAIVAVVHPIIPIAVSVYIPIWVLCAPKAPKAPESPICLPSPNLSPLTMF 254

DB 120 SYNSATIAVAVVHPIIPIAVSVYIPIWVLCAPKAPKAPESPICLPSPNLSPLTMF 179

0Y 255 VAVVIFAI WATNLTGLAVAINPDMAPQIPSELEVISYLLAFNSCLNAIVYGLLNON 314

DB 180 VAVVIFAI WATNLTGLAVAINPDMAPQIPSELEVISYLLAFNSCLNAIVYGLLNON 239

0Y 315 FPEREPRITLALMNPRLIQLASKOSH AEDUQSAAPP11 350  
 DB 240 FPEREPRITLALMNPRLIQLASKOSH AEDUQSAAPP11 355

RESULT: 10

US-08-896-365-8  
 Sequence 8, Application US/08896365  
 Patent No. 5939264

# GENERAL INFORMATION:

APPLICANT: Rohnschild, Max F.  
 APPLICANT: Tardif, Christopher K.  
 APPLICANT: Messer, Lori A.  
 APPLICANT: Tun-Ping, Yu  
 TITLE OF INVENTION: GENES AND GENETIC MARKERS FOR IMPROVED  
 TITLE OF INVENTION: REPRODUCTIVE TRAITS IN ANIMALS  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSER: Tardif, M-Ken, Thibault, Vachon & Seave  
 STREET: 801 Grand Avenue, Suite 3200  
 CITY: Des Moines  
 STATE: Iowa  
 COUNTRY: USA  
 ZIP: 50309

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOURCEWARE: Patent In Release #10, Version #1 30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08896365  
 FILING DATE: 18-JUL-1997

CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/022,180  
 FILING DATE: 18-JUL-1996

ATTORNEY/AGENT INFORMATION:  
 NAME: Nebel, Heidi S.  
 REGISTRATION NUMBER: 37,719  
 REFERENCE/AGENT NUMBER: 15896/211991

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 515-288-3667  
 TELEFAX: 515-288-1338

INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 257 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single

TOPOLOGY: unknown  
 MOLECULE TYPE: cDNA  
 HYPOTHEICAL: NO

ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Bos taurus  
 CELL TYPE: Melanocyte

US-08-896-365-8

Query Match 43.8%; Score 835; DB 2; Length 257;  
 Best Local Similarity 59.5%; Pred. No. 9.4e-62;

Matches 153; Conservative 43; Mismatches 61; Indels 0; Gaps 0;

0Y 94 YELLIVAFYDQALGEGHCKASAFVMSI SVIGSVFNITAI AINRYCYIHSKMAHYRIYR 153

DB 1 YELLIVAFYDQALGEGHCKASAFVMSI SVIGSVFNITAI AINRYCYIHSKMAHYRIYR 153

0Y 154 RHTPLHICLIMLITVALLPNPFVGSLEDPRIYSCFTQIATSTOYTAIVAVVHPIIPI 213

DB 61 SYNSATIAVAVVHPIIPIAVSVYIPIWVLCAPKAPKAPESPICLPSPNLSPLTMF 120











GenCore version 4.5  
Copyright (c) 1991-2000 GenProbes Ltd

OM Protein - protein search, using sw model

Run on: February 18, 2001, 14:20:54 : Search time 54.25 seconds  
(without alignments)  
388,150 Million cells updated, 300

Title: US-09-226-046-16  
Perfect score: 1908  
Sequence: 1 MSSENSANCTEAGGMAVFF.....ELASAPFPIISVHUALAL 362

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DR seq length: 0  
Maximum DR seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: PIR-661\*  
1: PIR1\*  
2: PIR2\*  
3: PIR3\*  
4: PIR4\*

pred No. is the number of results predicted by theory to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query Match	Length	DB ID	Description
1	1908	100.0	362	138990	Mel1b-melatonin re
2	1123	58.9	420	151100	Mel1c receptor su
3	1108.5	58.1	289	572554	Melatonin receptor
4	1088	57.0	350	148945	Mel-1a melatonin r
5	1048	54.9	366	146469	Mel-1a melatonin r
6	854.5	44.8	614	879450	Melatonin receptor
7	546	28.6	156	184498	Melatonin receptor
8	542	28.4	156	162107	Melatonin receptor
9	340	17.8	384	A45490	neuropeptide Y/pep
10	337.5	17.7	363	157965	neuropeptide Y/pep
11	337.5	17.7	364	150763	somatostatin recep
12	337	17.7	349	S12863	somatostatin recep
13	337	17.7	382	S17368	neuropeptide Y rec
14	337	17.7	392	R44114	neuropeptide Y/pep
15	330.5	17.3	388	JN0605	somatostatin recep
16	324	17.0	344	A17219	crata-speciatic scm
17	320	16.8	380	A55229	kappa opioid recep
18	318.5	16.7	391	A11795	somatostatin recep
19	316	16.6	384	JC4629	somatostatin recep
20	314	16.5	381	174360	hypothalamic recep
21	314.5	16.5	391	C41795	somatostatin recep
22	313	16.4	391	A19297	somatostatin recep
23	312	16.4	375	139182	neuropeptide Y/pep
24	311	16.3	375	G22300	pancreatic polypod
25	310.5	16.3	369	D41795	somatostatin recep
26	310	16.2	462	A15896	beta-adrenergic ic
27	309.5	16.2	346	S29248	somatostatin recep
28	309.5	16.2	560	A38741	alpha-1A adrenergic
29	308	16.1	369	A45291	somatostatin recep

30	308	16.1	515	2	A40491	alpha-1-adrenergic
31	307.5	16.1	349	2	I59336	galanin receptor 1
32	307	16.1	423	2	P49470	glucocorticoid-ind
33	306	16.0	400	2	S32804	beta-3-adrenergic
34	306	16.0	517	2	A45121	alpha-1B adrenergic
35	305.5	16.0	440	2	A44081	alpha-1B adrenergic
36	304.5	16.0	370	1	I52115	G protein-coupled
37	303	15.9	365	2	I52083	somatostatin recep
38	302.5	15.9	369	2	R41795	somatostatin recep
39	302.5	15.9	369	2	S56643	opioid receptor mu
40	302.5	15.9	407	1	T02374	neurokinin 1 recep
41	302.5	15.8	389	2	A57310	mu opioid receptor
42	300.5	15.7	420	2	I56554	mu opiate receptor
43	300	15.7	386	2	I52338	kappa opioid recep
44	300	15.7	428	2	A55044	beta-4-adrenergic
45	299.5	15.7	398	2	I56517	mu opioid receptor

## ALIGNMENTS

RESULT 1  
138990  
Mel1b-melatonin receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 31-May-1990, rev:revise-revision 01-May-1990, rev:01-May-1990  
C:Accession: I38990  
R:Peptide: S.M.: Gadsden, C.J. Mahler, C.D. Weaver, D.P.: Sladenhaugh, S.A.: Gosselin,  
Proc. Natl. Acad. Sci. U.S.A. 92: 8744-8748, 1995  
ATTN: Molecular characterization of a novel melatonin receptor expressed in human  
A:Reference number: 138990, MIMD:46004613  
A:Accession: I38990  
A:Status: preliminary, translated from CD,EMBL,TrEMBL  
A:Molecule type: mRNA  
A:Residues: 1-362 <PEP>  
A:Cross-species: EMBL:05341, NID:947109, PIR:AC060412, NID:9471194  
C:Superfamily: vertebrate rhodopsin

Query Match	100.0%	Score 1908	DB 2	Length 362
Best Local Similarity	100.0%	pred No 1e-156		
Matches 362	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MSSENSANCTEAGGMAVFFPSWSASASRRSRTPRPWAPAKISAVITVAVVGNLL 60		
DE	1	MSSENSANCTEAGGMAVFFPSWSASASRRSRTPRPWAPAKISAVITVAVVGNLL 60		
QY	51	VILSVLSKRLKNGNLFVLSLALCEVAVFYPPIIVAVFVLSALDEEHAKASAPVM 120		
DE	51	VILSVLSKRLKNGNLFVLSLALCEVAVFYPPIIVAVFVLSALDEEHAKASAPVM 120		
QY	121	GLSVAGSVENITAIINPYCYICSHMAVHPYRPMHTPIHFLTLITVAAILPNFVSS 180		
DE	121	GLSVAGSVENITAIINPYCYICSHMAVHPYRPMHTPIHFLTLITVAAILPNFVSS 180		
QY	121	LEVYFRTISCFITASTCYTAAVVHEFLFVAVSFYPIYVAVIIVQAPKAPFSP 240		
DE	121	LEVYFRTISCFITASTCYTAAVVHEFLFVAVSFYPIYVAVIIVQAPKAPFSP 240		
QY	241	GLKSLSSPLTFVFEVIFALQAPLNLGLAVAINPQMAVQFPEHFLVSYLAVFN 300		
DE	241	GLKSLSSPLTFVFEVIFALQAPLNLGLAVAINPQMAVQFPEHFLVSYLAVFN 300		
QY	361	SLNAIVGLNLPPEYKHLIATMNPQHTVQASKSHAKVQSPAPPTIVQAGND 360		
DE	361	SLNAIVGLNLPPEYKHLIATMNPQHTVQASKSHAKVQSPAPPTIVQAGND 360		
QY	361	AL 362		
DE	361	AL 362		

151664

Melatonin receptor subtype - African clawed frog

C.Species: Xenopus laevis (African clawed frog)

C.Date: 13-Sep-1994; sequence\_revision 13-Sep-1995; #text\_change 21-Jul-2000

C.Accession: U51666

C.Description: 13: Kanno, S.; Iwamoto, M. P.; Peppert, S. M.

C.Reference: Natl. Acad. Sci. U.S.A. 91, 6133-6137, 1994

C.Title: Expression cloning of a high-affinity melatonin receptor from Xenopus dermal melanocytes

C.Reference number: U51666; MIMD:94486591

Accession: U51666

Accession: preliminary; translated from GB/EMBL/DBJ

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

Accession: U51666

C:Superfamily: vertebrate rhodopsin

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

Best Local Similarity 59.48; Prod No 3 9e-89

Matches 205; Conservative 59; Mismatches 79; Indels 10; Gaps 3

Query Match 59.98; Score 1123; DB 2; Length 420

## RESULT 5

146459

Mel-1a melatonin receptor - sheep

C:Species: Ovis orientalis aries, Ovis aries (domestic sheep)

C:Date: 19-Dec-1997 #sequence\_revision 19-Dec-1997 #text\_change 17-Mar-2000

C:Accession: 146459

R:Reppert, S.M.; Weaver, D.R.; Ebisawa, T.

Neuron 13, 1177-1185, 1994

A:Title: Cloning and characterization of a mammalian melatonin receptor that mediates re

A:Reference number: 138848. MID:9503233

A:Accession: 146459

A:Status: preliminary (transcribed from cDNA)

A:Molecule type: mRNA

A:Residues: 1-366 &lt;REP&gt;

A:Cross-references: EMBL:U14104; NID:9503233; FID:AA61721.1; FID:9503232

C:Superfamily: vertebrate rhodopsin

Query Match

54.9% Score 1048; DB 2; Length 366;

Best Local Similarity 58.1% Pred. No. 9.6e-83;

Matches 205; Conservative 58; Mismatches 74; Indels 16; Gaps 5;

CY 4 NCSEA--NCCEGGAAGVAPPGSGAGSAPPPTPPPPVAPALSVLLVTTAVVGNLLV 61

DB 16 NGSSALLVNSOA-----PGAGD---GVPPSPSWLAATLSTLFTTVVTVVNLV 64

CY 62 ILTVLPNPKLPAGNLTVSLALAVVAVYPPPLIIVIPYDGMATGEPHCAAFVWG 101

DB 65 VLSVPNKKLRASGVFVSLAVAPLVAVPYPLAASVNNWSLSLHCLSTELM 124

CY 122 LSVIGSVNTAIAINPYCYICHSMAHYRPMHTPLHICLLVLLTVALLFEPVGL 181

DB 125 LSVIGSVNTAIAINPYCYICHSMAHYRPMHTPLHICLLVLLTVALLFEPVGL 184

CY 142 EYDPIVSTCT 241

DB 145 EYDPIVSTCT 244

CY 242 LKPSLST 301

DB 245 LKPSLST 304

CY 302 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 353

DB 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 356

CY 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 353

DB 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 356

CY 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 353

DB 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 356

CY 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 353

DB 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 356

CY 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 353

DB 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 356

CY 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 353

DB 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 356

CY 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 353

DB 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 356

CY 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 353

DB 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 356

CY 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 353

DB 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 356

CY 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 353

DB 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 356

CY 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 353

DB 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 356

CY 305 CLNATVCLLNQNPPEKPTLLALWNPFCITQASGSH-ABSLSQSPAPPI 353

CY 88 VAAFPYPLLVAFYDGMALGEGHCAAFVWGLSVIGSVNTAIAINPYCYICHSMA 147

DB 76 LVATPYPLLVAFYDGMALGEGHCAAFVWGLSVIGSVNTAIAINPYCYICHSMA 135

CY 148 YHPTVPMWHPPLHICLLVLLTVALLFEPVGLSTCTCTCTCTCTCTCTCTCT 207

DB 146 YHPTVPMWHPPLHICLLVLLTVALLFEPVGLSTCTCTCTCTCTCTCTCTCT 195

CY 208 HPLPIAVNSCYLRIVLVLOARRKA--KPSRLCLKPSDLRSFLTMFVVFALICA 265

DB 196 HPLPIAVNSCYLRIVLVLOARRKA--KPSRLCLKPSDLRSFLTMFVVFALICA 251

CY 266 PLNCTGAVANPEEMAPLCTFGCTVTVCAAFNSQINAVYCTIENPPEKPTLLA 325

DB 262 PLNCTGAVANPEEMAPLCTFGCTVTVCAAFNSQINAVYCTIENPPEKPTLLA 311

CY 326 LMPN 329

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

CY 312 MRHP 315

DB 312 MRHP 315

[illegible][illegible]











GenInfo version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd

SW protein - protein search, using sw model

Run on February 18, 2001 14:36:34 Search time 51.08 seconds  
(without alignments)  
214 977 Million cell updates/sec

Title: US-09-226-046-16

Perfect score: 1908  
Sequence: 1 MSNENSFANCCFRCAGAVP.....EGLSPAPPIVCHQAL 362

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 98757

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt\_39\*

Prod No is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed  
and is derived by analysis of the total score distribution

## SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description
1	1908	100.0	362	1	MLIB_HUMAN	P49286 homo sapien
2	1142	59.9	346	1	MLIC_CHICK	P49286 gallus gall
3	1123	58.9	420	1	MLIC_XENLA	P49286 xenopus lae
4	1122.5	58.9	353	1	MLIA_CHICK	P49285 gallus gall
5	1112	58.8	363	1	MLIA_PHEX	P49285 pheopus sp
6	1108.5	58.1	280	1	MLIR_CHICK	P49286 gallus gall
7	1088	57.0	350	1	MLIR_HUMAN	P49286 homo sapien
8	1072.5	56.2	353	1	MLIA_MOUSE	P49286 mus musculu
9	1048	54.9	366	1	MLIA_SHEEP	P49286 ovine aries
10	874.5	44.8	613	1	MLIX_HUMAN	P49286 homo sapien
11	846	44.3	575	1	MLIX_SHEEP	P49286 ovine aries
12	837.5	43.9	583	1	MLIX_MOUSE	P49286 mus musculu
13	835	43.8	257	1	MLIA_PHEX	P49285 pheopus sp
14	584	30.6	152	1	MLIB_XENLA	P51051 xenopus lae
15	577	29.2	153	1	MLIB_PHEX	P49286 pheopus sp
16	542	28.4	156	1	MLIA_PAT	P49286 ratius norv
17	533	27.3	157	1	MLIB_PHEX	P51051 xenopus lae
18	531	27.8	157	1	MLIA_PHEX	P49286 pheopus sp
19	523	27.4	157	1	MLIA_PHEX	P51046 brachydanio
20	517	27.1	120	1	MLIR_PAT	P49287 ratius norv
21	511	26.8	154	1	MLIA_PIG	P00281 sus scrofa
22	502.5	26.3	157	1	MLIX_PHEX	P49285 pheopus sp
23	434.5	22.8	153	1	MLIA_XENLA	P51048 xenopus lae
24	341	17.9	383	1	MLIR_PHEX	P49286 pheopus sp
25	340	17.8	384	1	MLIR_PHEX	P49286 pheopus sp
26	339	17.8	384	1	MLIR_PHEX	P49286 pheopus sp
27	339	17.8	383	1	MLIR_PHEX	P49286 pheopus sp
28	337.5	17.7	384	1	MLIR_PHEX	P49286 pheopus sp
29	337	17.7	382	1	MLIR_PHEX	P49286 pheopus sp
30	337	17.7	382	1	MLIR_PHEX	P49286 pheopus sp
31	330.5	17.3	388	1	MLIR_PHEX	P49286 pheopus sp
32	329.5	17.3	371	1	MLIR_PHEX	P49286 pheopus sp
33	324	17.0	384	1	MLIR_PHEX	P49286 pheopus sp

34	320	16.8	380	1	MLIR_PHEX	P49286 pheopus sp
35	318.5	16.7	346	1	MLIR_PHEX	P49286 pheopus sp
36	318.5	16.7	391	1	MLIR_PHEX	P49286 pheopus sp
37	316.5	16.6	369	1	MLIR_PHEX	P49286 pheopus sp
38	316	16.6	384	1	MLIR_PHEX	P49286 pheopus sp
39	315.5	16.5	391	1	MLIR_PHEX	P49286 pheopus sp
40	314.5	16.5	391	1	MLIR_PHEX	P49286 pheopus sp
41	313	16.4	381	1	MLIR_PHEX	P49286 pheopus sp
42	312	16.4	375	1	MLIR_PHEX	P49286 pheopus sp
43	310.5	16.3	382	1	MLIR_PHEX	P49286 pheopus sp
44	310	16.2	483	1	MLIR_PHEX	P49286 pheopus sp
45	308	16.1	469	1	MLIR_PHEX	P49286 pheopus sp

## ALIGNMENTS

RESULT	ID	MLIB_HUMAN	STANDARD	PRT	362 AA
1	AC	P49286			
DT	01-FEB-1996	(rel. 33, Created)			
DT	01-FEB-1996	(rel. 33, Last sequence update)			
DT	01-FEB-2000	(rel. 40, Last annotation update)			
DE	MELANIN RECEPTOR TYPE 1B (MEL-1B-R)				
GN	MIR1B				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo				
BN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-96004618; PubMed-7568007;				
PA	Pepper S M, Godson G, Mahle C D, Weaver D P,				
PA	Staugenhardt S A, Gusella J F:				
PT	"Molecular characterization of a second melanin receptor expressed				
PT	in human retina and brain: the Mel1b melanin receptor."				
PL	Proc. Natl. Acad. Sci. U.S.A. 92:8734-8738(1995).				
RN	[2]				
RP	SEQUENCE FROM N.A. AND VARIANTS G11-24 AND PHR-66.				
RX	MEDLINE-20159877; PubMed-10696804;				
PA	Erstawa T, Nohiyama M, Kajimura N, Kamei Y, Shibui K, Kim K,				
PA	Kudo Y, Iwase T, Sugishita M, Jodoi T, Ikeda M, Ozeki Y,				
PA	Maruyama T, Sakimura M, Kato M, Yamada N, Toyoshima F, Okawa M,				
RA	Takahashi K, Yamuchi T:				
RT	"Genetic polymorphisms of human melanocyte receptor gene in				
RT	circadian rhythm sleep disorders and controls."				
RT	Neurosci. Lett. 290:29-32(2000).				
CC	-1- FUNCTION: HIGH AFFINITY RECEPTOR FOR MELANIN. IT MEDIATES				
CC	THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELANIN. THE ACTIVITY				
CC	OF THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G				
CC	PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN RETINA AND TESTIS IN BRAIN AND				
CC	HIPPOCAMPUS.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. Their aim is to preserve up its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement. (see <a href="http://www.isdb.org">http://www.isdb.org</a> )				
CC	or send an email to <a href="mailto:license@isdb.org">license@isdb.org</a> .				
CC	EMBL: U03341; AAC50610.1;				
CC	EMBL: ABC3598; BAA92315.1;				
CC	EMBL: ABC3597; BAA92315.1; JOINED.				
CC	GENB: G002022;				
CC	MM: K00804;				
CC	INTERPRO: IPR000026;				
CC	INTERPRO: IPR000276;				
CC	PFAM: PF00001; 7tm_1; 1.				
CC	PRINTS: F00027; PROPHOSPHON.				









```

50 LVLSVLPKRLPNAGNLFLVSLAI ANLVAVPYPLILVAIFYDGMALGEEHCKASAFV 119
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
50 LVLSVYRKRLKLPNAGNLFLVSLAIADIVALLPYPLVITSFNNGNLGLVHQCISFL 109
2Y 120 MCLSVIGSFNTAIAINRYVYIGSMAYHRZYPPMHPILICILWLTVALLFNEVG 179
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 110 MGLSVIGSFNTGIAINRYVYIGSLKYDRFLYSKNKSACGYFLWLTVALIMENLDTG 169
2Y 180 SLEVDRIASCTFIOTASTOYTAAVVTHFLIPVAFSCYPLIVVYLVQAPKAPKPSR 239
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 170 TICVDPRITSCFTQSVSAVITAVVHFVPMITVIFCTYIRIWLTVLQVPPKPPK 229
2Y 240 LCLPSPDRPSFTMVFYVFAICVAPLNCICLAVAINFQEMAPQIPSEILVIZELLAVF 239
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 230 PRLKPDGFNFVMTVEVFLFAICVAPLNFILGLIVASDPATAPRIPEMLVVASVYNAVF 289
QY 300 NSCLNIVVGLINQNPPEYKPIITAIKMPKPIQDASKGSABEILSPAPPI 352
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 290 NSCLNIVVGLINQNPPEYKPIITAIKMPKPIQDASKGSABEILSPAPPI 342

RESULT 6
MLIB_CHICK STANDARD PRT: 289 AA.
ID MLIB_CHICK STANDARD PRT: 289 AA.
AC P51050.
DI 01-OCT-1996 (Rel. 34, Created)
DI 01-OCT-1996 (Rel. 34, Last sequence update)
DI 01-OCT-1996 (Rel. 34, Last annotation update)
DE MELANOTIN RECEPTOR TYPE 1R (MEL-1R) (EPHRAIM)
OS Gallus gallus (Chicken)
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Archosauria: Aves: Neornithae: Galliformes: Phasianidae: Phasianinae:
OC [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-96063731; PubMed-7589552;
RA Liu F., Yuan H., Sugamori K.S., Hamadanizadeh A., Lee F.T.S.,
RA Pang S.F., Brown G.M., Pilsbury D.A., Niznik H.R.;
RT "Molecular and functional characterization of a partial cDNA encoding
RT a novel chicken brain melatonin receptor."
RL FEBS Lett. 374:273-278(1995).
CC
CC FUNCTION: HIGH AFFINITY RECEPTOR FOR MELANOTIN. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY PERUSSIS TOXIN SENSITIVE G PROTEINS
CC THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).
CC SUBCELLULAR LOCATION: INTERSPAL MEMBRANE PROTEIN.
CC TISSUE SPECIFICITY: BRAIN AND KIDNEY. WITH IPACF LEVUS IN DRUGS
CC SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announc/
CC or send an email to license@sib-sib.ch)
CC
DR FMRI: 106609; AAAR5008 1.
DR HSSP: P54725; 10BA.
DR GCRDB: GCR_10A2.
DR INTERPRO: IPR000276.
DR PIRAM: PRO0001; 7m.1.1.
DR PROSITE: PS00237; G-PROTEIN_PROCE.F1.1.
DR PROSITE: PS00242; G-PROTEIN_PROCE.F1.2.
KW G-protein coupled receptor; Transmembrane; glycoprotein
FT DOMAIN 1 2 CYTOPLASMIC (POTENTIAL)
FT TRANSMEM 3 23 2 (POTENTIAL)
FT DOMAIN 24 41 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 42 62 3 (POTENTIAL)
FT DOMAIN 63 81 CYTOPLASMIC (POTENTIAL)
FT TRANSMEM 82 102 4 (POTENTIAL)

```

```

FT DOMAIN 103 126 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 127 147 5 (POTENTIAL)
FT DOMAIN 148 179 CYTOPLASMIC (POTENTIAL)
FT TRANSMEM 180 200 6 (POTENTIAL)
FT DOMAIN 201 213 EXTRACELLULAR (POTENTIAL)
FT TRANSMEM 214 234 7 (POTENTIAL)
FT DOMAIN 235 289 CYTOPLASMIC (POTENTIAL)
FT DISULFID 39 116 BY SIMILARITY
SQ SEQUENCE 289 AA; 33001 MW; 08F0E3E15B3FE1 CNO64;

Query Match 59.1%; Score 1158.5; E: 1e-1; 1000th 289;
Best local similarity 72.2%; Prod No 14e-69;
Matches 205; Conservative 33; Mismatches 45; Indels 1; Gaps 1;

QY 75 GULFVSLADLVVAFAPYPLILVAIFYDGMALGEEHCKASAFVMLSTVSGSFNTAI 134
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GNAFVSLADLVVAFVLPYPLILVAIFHNSMTGEGHCKVSGVMSLSTVSGSFNTAI 60
QY 136 AINRYVYIGSMAYHRZYPPMHPILICILWLTVALINFPVNSLEDPKPYSCFTIQ 194
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AINRYVYIGSMAYHRZYPPMHPILICILWLTVALINFPVNSLEDPKPYSCFTIQ 120
QY 195 TASTQYTAAVVTHFLIPVAFSCYPLIVVYLVQAPKAPKPSRIQAKRSIRPSITMF 254
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 TASQYTAAVVTHFLIPVAFSCYPLIVVYLVQAPKAPKPSRIQAKRSIRPSITMF 180
QY 255 VVVFVFAICVAPLNCICLAVAINFQEMAPQIPSEILVIZELLAVFNSCLNIVVGLINQ 314
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 VVVFVFAICVAPLNCICLAVAINFQEMAPQIPSEILVIZELLAVFNSCLNIVVGLINQ 240
QY 315 FPEYKPIITAIKMPKPIQDASKGSABEILSPAPPIIGVDD 358
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 FPEYKPIITAIKMPKPIQDASKGSABEILSPAPPIIGVDD 283

RESULT 7
MLIB_HUMAN STANDARD PRT: 350 AA.
ID MLIB_HUMAN STANDARD PRT: 350 AA.
AC P48039.
DI 01-FEB-1996 (Rel. 33, Created)
DI 01-FEB-1996 (Rel. 33, Last sequence update)
DI 01-OCT-2000 (Rel. 40, Last annotation update)
DE MELANOTIN RECEPTOR TYPE 1A (MEL-1A-R).
GN MTNRIA.
OS Homo sapiens (Human).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo
OC [1]
RN
RP SEQUENCE FROM N.A.
RX MEDLINE-95033233; PubMed-7946354;
RA Peppert S.W., Weaver D.P., Epstein T.;
RT "Cloning and characterization of a mammalian melatonin receptor that
RT mediates reproductive and circadian responses."
RL Neuron 13:1177-1185(1994).
CC
CC SEQUENCE FROM N.A. AND VARIANTS 15P-54 AND VAL-157.
PC TISSUE-LEUKOCYTE;
RX MEDLINE-99400459; PubMed-10471411;
RA Ebisawa T., Kajimura N., Uchiyama M., Katoh M., Sekimoto M.,
RA Marabe T., Ozeki Y., Ikeda M., Imai T., Saitoh M., Iwase T.,
RA Kamei Y., Kim K., Shibui K., Kudo Y., Yamada N., Toyoshima F.,
RA Okawa M., Takahashi K., Yamauchi T.;
RT "Allele variants of human melatonin 1a receptor: function and
RT prevalence in subjects with circadian rhythm sleep disorders."
RT Biochem. Biophys. Res. Comm. 262:932-937(1999).
CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR MELANOTIN. LIKELY TO MEDIATES
CC THE REPRODUCTIVE AND CIRCADIAN ACTIONS OF MELANOTIN. THE ACTIVITY
CC OF THIS RECEPTOR IS MEDIATED BY PERUSSIS TOXIN SENSITIVE G
CC PROTEINS THAT INHIBITS ADENYLATE CYCLASE ACTIVITY.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN HYPOTHALAMIC PARS TUBERIALIS AND
CC HYPOTHALAMIC SUPRACHIASMATIC NUCLEI (SNIC). HIPPOCAMPUS.

```







FT DOMAIN 210 239 CYTOPLASMIC (POTENTIAL)  
 FT TRANSMEM 240 260 6 (POTENTIAL)  
 FT DOMAIN 261 273 7 (POTENTIAL)  
 FT TRANSMEM 274 294 7 (POTENTIAL)  
 FT DOMAIN 295 575 CYTOPLASMIC (POTENTIAL)  
 FT DISULFID 101 178 BY SIMILARITY  
 FT CONFLICT 138 138 P - S L (IN PER 2)  
 FT CONFLICT 158 158 I - S M (IN PER 2)  
 FT CONFLICT 218 220 ASD - S D (IN PER 2)  
 SQ SEQUENCE 575 AA: 62809 MW: 62041 CIPEDDF8 CPGC4.

Query Match 44 38 Score 846 DB 1 Length 575  
 Best Local Similarity 45.84 Pval No 2.5e-51  
 Matches 150: Conservative 80: Mismatches 72: Indels 18: Gaps 4:

QY 36 PPMVAPASAVLITVAVVGNLITVLSVLPNPKLKNAGNLTSLALADLVAVVAPP 96  
 DB 24 PVALVPMFCAMVITVLLVLSNSVITAVSKNKLNSNVSVLSVALMLVAVPP 53  
 QY 96 LILVAIFDGMALGEBCKASAFVWGLSVGSVFNTAIAINRYCYCHSMVPTVPPW 165  
 DB 84 LMLHMAIGMDISKLGQGMWGLTGLSVASIFNMAIAINRYCYCHSLGVPTSPSP 143  
 QY 156 HTPHICITWLTIVALLPNFVSGLEDPRTYSCITITQASTQYTAADVHTFLLPVAV 215  
 DB 144 NTCIYLAIVTMTVLAIVLPNNYIGTIEYDPRTYCIENYNNNAFAVTICVHPVLLI 203  
 QY 216 VSPCYLPIWLVLCAPKPA--KPSPLCTKPSLPSLTVEYVFIQWALNCGSLA 272  
 DB 274 VGFVYVKTMTVLAAPDAPAGNPNGL----ATVPRNLTNFIPLFAVWCIYNLTVL 259  
 QY 274 VAINQEMAPDIPGGLVSTYLLAVFNSCINAIYVGLLNONPREKPKILLALMP---- 329  
 DB 260 VAVNPKEMAGKIPWVYLAIVFVNSCINAIYVGLLNONPREKPKILLALMP---- 319  
 QY 330 -----RHCIODASKGSHA 342  
 DB 320 SGLIDVRE-MQEAQAHHA 338

RESULT 12  
 MIX\_MOUSE  
 ID MIX\_MOUSE STANDARD PRT 693 AA  
 AC 098495:  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 01-JUL-2000 (Rel. 40, Last annotation update)  
 DE MELATONIN-RELATED RECEPTOR (H9)  
 GN GPR50  
 OS Mus musculus (Mouse)  
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 NC Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.  
 RN [1]  
 RP MEDLINE-99134305: Pubmed-9933574:  
 RA Gubitz A.K., Reppert S.M.:  
 RI "Assignment of the melatonin-related receptor to human chromosome X  
 (GPR50) and mouse chromosome X (GPR50)."

CC -1- FUNCTION: DOES NOT BIND MELATONIN.  
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC This SWISS-PROT entry is copyright © 1999 by the Swiss Institute of Bioinformatics  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation.  
 CC The European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed, changed by and for commercial  
 CC entities requires a license agreement. (See help /www.sdbioinformatics.org)  
 CC or send an email to license@sdbioinformatics.org

CC EMBL: AF065145: AAC23462.1: ALT\_INIT  
 DB

DB MGI: 1333877, GPR50.  
 DB INTERPRO: IPR00276:  
 DB INTERPRO: IPR00276:  
 DB PPM: PPM0001, 7tm1.1.  
 DB PRINTS: PRO1816, MELATONINR  
 DB PROSITE: PS00237, G-PROTEIN\_RECEP\_F1\_1:  
 DB PROSITE: PS00262, G-PROTEIN\_RECEP\_F1\_2\_1:  
 KW G-protein coupled receptor, Transmembrane, Extracellular, Potential.  
 FT TRANSMEM 32 51 1 (POTENTIAL)  
 FT DOMAIN 52 64 CYTOPLASMIC (POTENTIAL)  
 FT TRANSMEM 65 85 2 (POTENTIAL)  
 FT DOMAIN 86 103 EXTRACELLULAR (POTENTIAL)  
 FT TRANSMEM 104 124 3 (POTENTIAL)  
 FT DOMAIN 125 143 CYTOPLASMIC (POTENTIAL)  
 FT TRANSMEM 144 164 4 (POTENTIAL)  
 FT DOMAIN 165 188 EXTRACELLULAR (POTENTIAL)  
 FT TRANSMEM 189 209 5 (POTENTIAL)  
 FT DOMAIN 210 239 6 (POTENTIAL)  
 FT TRANSMEM 240 260 7 (POTENTIAL)  
 FT DOMAIN 261 273 EXTRACELLULAR (POTENTIAL)  
 FT TRANSMEM 274 294 7 (POTENTIAL)  
 FT TRANSMEM 295 583 CYTOPLASMIC (POTENTIAL)  
 FT DISULFID 101 178 BY SIMILARITY  
 SQ SEQUENCE 583 AA: 64330 MW: 63553 QBSAL42 JF564:

Query Match 43.9% Score 837.5 DB 1 Length 583:  
 Best Local Similarity 47.8% Pval No. 9.6e-51:  
 Matches 150: Conservative 77: Mismatches 72: Indels 15: Gaps 5:

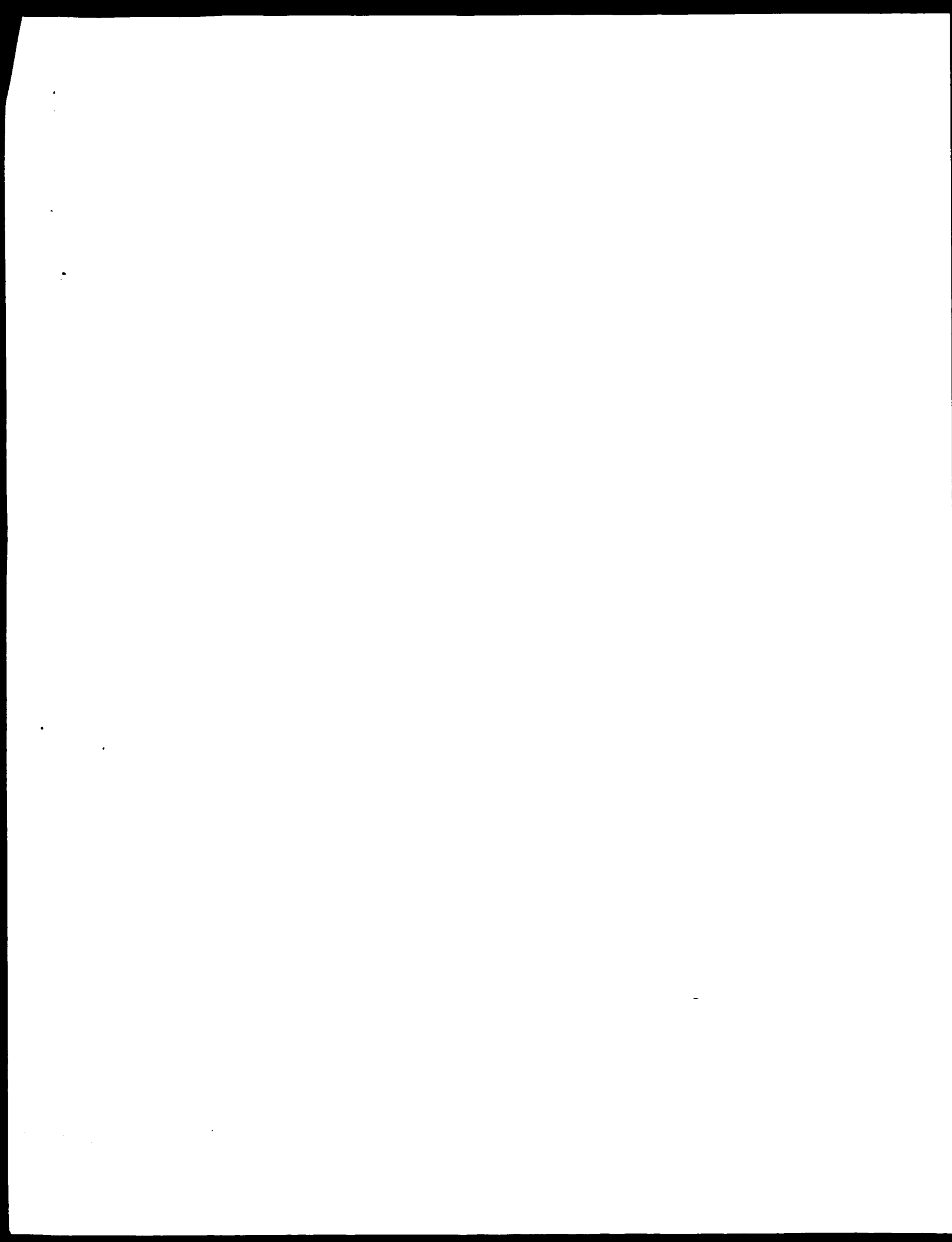
QY 32 PTPPPVAPAL-----SAVLITVAVVGNLITVLSVLPNPKLPNANFIIVSLALNI 87  
 DB 17 KLEPDEV-PPALIFEMFCAMVITVLLVLSNSVITAVSKNKLNSNVSVLSVALM 75  
 QY 88 VVARYPYLITVAIFDGMALGEBCKASAFVWGLSVGSVFNTAIAINRYCYCHMA 147  
 DB 76 LVATPYPLMLNVSAGWGLSLQGMWGLTGLSVASIFNMAIAINRYCYCHSLQ 135  
 QY 148 YHPIPPWHTPHICITWLTIVALLPNFVSGLEDPRTYSCITITQASTQYTAADVHT 207  
 DB 136 YKPIPSLRNICITVMTVLAIVLPNNYIGTIEYDPRTYCIENYNNNAFAVTICV 104  
 QY 208 HPLITVAVSPCYLPIWLVLCAPKPA--KPSPLCTKPSLPSLTVEYVFIQWALN 272  
 DB 196 HFAVPLLVGYCYIKIKIVLAIVFVNSCINAIYVGLLNONPREKPKILLALMP 251  
 QY 265 PLNCTAVAINQEMAPDIPGGLVSTYLLAVFNSCINAIYVGLLNONPREKPKILL 225  
 DB 252 PVNVLIVAVIKEMAGKIPWVYLAIVFVNSCINAIYVGLLNONPREKPKILL 311  
 QY 226 LMPN-----RHCIOD 335  
 DB 312 MRBILFSLISD 325

RESULT 13  
 ID MIA\_BOVIN STANDARD PRT 257 AA  
 AC 004769:  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE MELATONIN RECEPTOR TYPE 1A (MEL-1A-R) (FRAGMENT)  
 GN MNFLA.  
 OS Bos taurus (Bovine)  
 OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 NC Mammalia: Eutheria: Cetartiodactyla: Fuminantia: Pecora: Bovidae:  
 RN [1]  
 RP MEDLINE-97262109: Pubmed-9107687:  
 RA TISSUE-HYPOTHALAMUS, AND PITUITARY:  
 DB



BT 15-JUL-1999 (Rel. 38, last annotation update)  
DE MELATONIN RECEPTOR TYPE 1B 22.6 (MEL-1B-R) (FRAGMENT).  
GN MEL1BR.  
CS Brachdario rerio (zebrafish) (zebra danio).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
CC Cypriniformes; Cyprinidae; Rasbora; Danio.  
RN 11  
RP SEQUENCE FROM N.A.  
RX MEDLINE-96073557; PubMed-7576645;  
FA Reppert S.M., Weaver D.R., Cassone V.M., Godson C.,  
FA Kolakowski L.F. Jr.;  
RT "Melatonin receptors are for the birds: molecular analysis of two  
RT receptor subtypes differentially expressed in chick brain.";  
FL Neuron 15:1003-1015(1995).  
CC 1-1 FUNCTION: HIGH AFFINITY RECEPTOR FOR MELATONIN. THE ACTIVITY OF  
CC THIS RECEPTOR IS MEDIATED BY PERTUSSIS TOXIN SENSITIVE G PROTEINS  
CC THAT INHIBITS ADENYLATE CYCLASE ACTIVITY (BY SIMILARITY).  
CC 1-1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.  
CC 1-1 SIMILARITY: HOMOLOGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: U31824; AAA92496.1;  
DR ZFIN: ZDB-GENE-990415-156; MEL1BR.  
DR INTERPRO: IPR000276;  
DR PFAM: PF00001; 7tm\_1; 1.  
DR PROSITE: PS00237; G-PROTEIN\_RECEP\_F1\_1; PARTIAL.  
DR PROSITE: PS50262; G-PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Transmembrane; Glycoprotein.  
FT 1  
FT NON\_TER 1  
FT DOMAIN 1  
FT TRANSMEM 14 34 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 35 58 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 59 79 5 (POTENTIAL).  
FT DOMAIN 80 111 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 112 132 6 (POTENTIAL).  
FT DOMAIN 133 145 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 146 >153 7 (POTENTIAL).  
FT NON\_TER 153 153  
SQ SEQUENCE 153 AA; 17486 MW; 3B642AB847554784 CRC64;  
  
Query Match 30.2%; Score 577; DB 1; Length 153;  
Best Local Similarity 70.4%; Pred. No. 2,2e-33;  
Matches 107; Conservative 19; Mismatches 26; Indels 0; Gaps 0;  
  
QY 143 CHSMAYHRYVPMHTPIHILWILTVVALPPEFVSLSEYDPRPIYSCFIQTASTQYTA 202  
DB 1 CHSFAYGRLCSEFRNLLVALIYVALILPPEFVSLSEYDPRVYSCFTQTASTSYTV 60  
QY 273 AVVYIHRIIPAVVSFYTPVWLVICAPKAPPEPDLCLKPSCLPSFLKPYVYITFAI 262  
DB 61 VVVVHFLVPLAVVTFYELRQWLVLIQVRKRVSEERSVPSDLRNFTMFVAVFLFAI 120  
QY 263 CWAPLNCIGLAVAINPOEMAPQIPEGIFVTSY 294  
DB 121 CWAPLNLIGLVAINPEVMAPEVEMLEFVVS 152

Search completed: February 18, 2001, 14:36:39  
Job time: 3256 sec





SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_  
Ar Unit: \_\_\_\_\_  
Phone Number 30 \_\_\_\_\_  
Serial Number: \_\_\_\_\_  
Examiner #: \_\_\_\_\_  
Date: \_\_\_\_\_  
Mail Box and Bldg/Room Location: \_\_\_\_\_  
Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.  
\*\*\*\*\*  
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched.  
Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or  
unity of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if  
known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_  
Inventors (please provide full names): \_\_\_\_\_  
Earliest Priority Filing Date: \_\_\_\_\_  
\*\*\*\*\*  
\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the  
appropriate serial number.

STAFF USE ONLY

Searcher	_____	NA Sequence (#)	3	STN	_____
Searcher Phone #	_____	AA Sequence (#)	3+1	Serial	_____
Searcher Location	2/6/21	Structure (#)	_____	Questel/Orbit	_____
Date Searcher Picked Up	2/6/21	Bibliographic	_____	Dr Link	_____
Date Completed	2/22/21	Litigation	_____	Lexis/Nexis	_____
Searcher Prep & Review Time	_____	Fulltext	_____	Sequence Systems	03
Clinical Prep Time	_____	Patent Family	_____	WWW/Internet	_____
Online Time	_____	Other	_____	Other (specify)	_____

PTO-1590 (1-2000)



STIC-Biotech/ChemLib

3/11/96

From: Pak, Michael  
Sent: Friday, February 02, 2001 2:17 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search 09/226.046

Sequence search - 2 month amendment due by 2/24/01  
App. # 09/226.046  
Result format: Paper.  
Title: High affinity melatonin receptors and uses thereof

Please search:

Search commercial and interference.

1) SEQ ID NO: 5, 6, 11, 12, 15, and 16. Reverse translate NO: 12

Thanks.

Mike Pak

Michael D. Pak  
305-7038  
CM-1, Rm. 10E13  
AU 1646 - USPTO

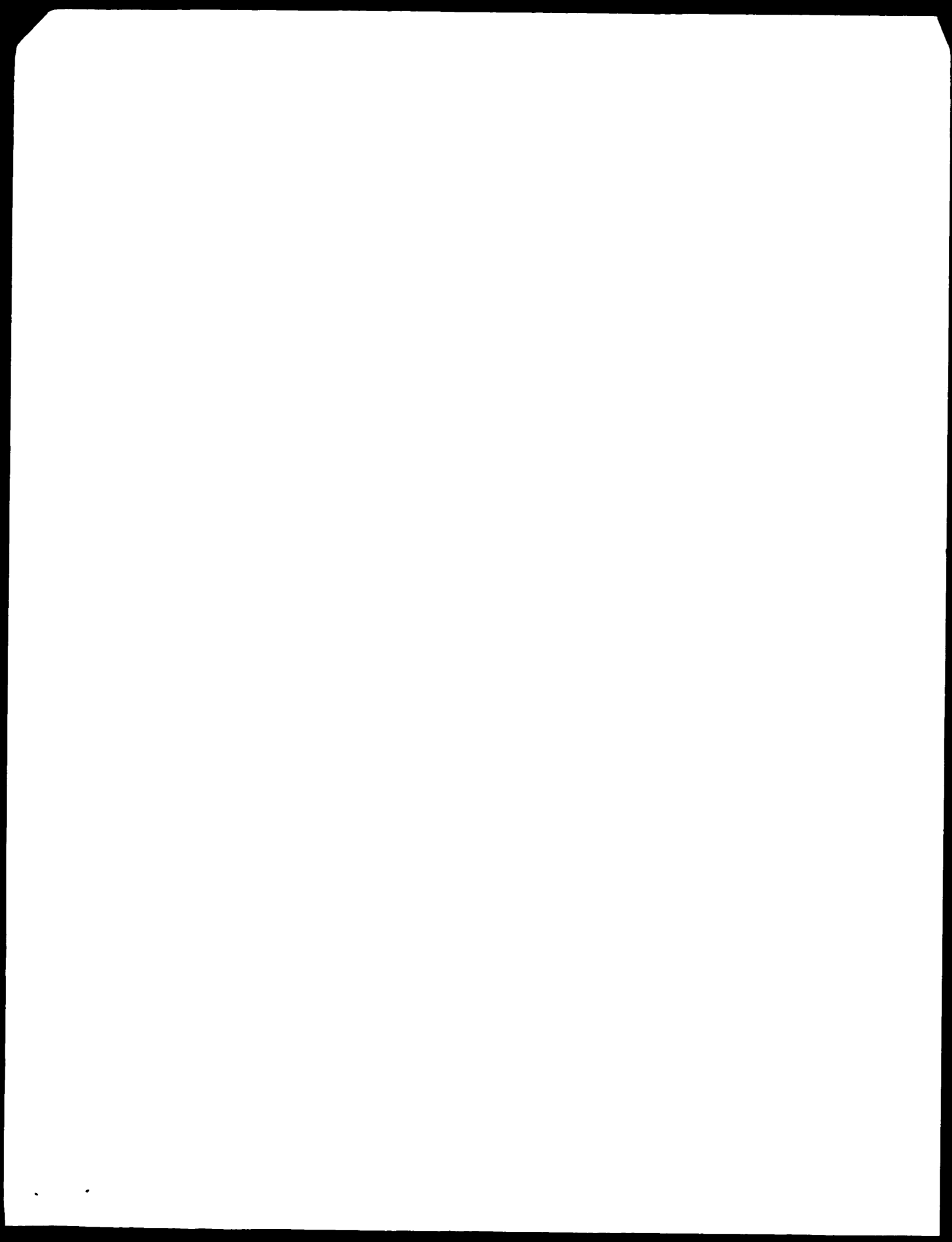


L9 ANSWER 1 OF 9 MEDLINE  
AN 92201186 MEDLINE  
TI The primary structure and gene organization of human substance P and neuropeptide Y receptors.  
AU Takahashi K; Tanaka A; Hara M; Nakanishi S  
CS Institute for Immunology, Kyoto University Faculty of Medicine, Japan.  
SO EUROPEAN JOURNAL OF BIOCHEMISTRY, (1992 Mar 15) 204 (3) 1025-33.  
CY GERMANY; Germany, Federal Republic of  
DT Journal; Article; (JOURNAL ARTICLE)  
LA English  
FS Priority Journals; Cancer Journals  
OS GENBANK-X65172; GENBANK-X65173; GENBANK-X65174; GENBANK-X65175; GENBANK-X65176; GENBANK-X65177; GENBANK-X65178; GENBANK-X65179; GENBANK-X65180; GENBANK-X65181  
EM 9207  
L9 ANSWER 2 OF 9 MEDLINE  
AN 91093253 MEDLINE  
TI The human neurokinin A (substance K) receptor. Molecular cloning of the gene, chromosome localization, and isolation of the cDNA from tracheal and gastric tissues.  
AU Gerard N P; Eddy R L Jr; Shows T B; Gerard C  
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1991 Jan 15) 266 (2) 1354.  
CY United States  
DT Errata; (PUBLISHED ERRATUM)  
LA English  
FS Priority Journals; Cancer Journals  
EM 9104  
L9 ANSWER 3 OF 9 MEDLINE  
AN 92060628 MEDLINE  
TI Cloning, expression of the human substance K receptor, and analysis of its role in mitogenesis.  
AU Cyr C; South V; Saltzman A; Felder S; Ricca G A; Jaye M; Huebner K; Kagan J; Croce C M; Schlessinger J; et al  
CS Department of Pharmacology, New York University School of Medicine, New York 10016.  
SO ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, (1991) 632 426-7.  
CY United States  
DT Journal; Article; (JOURNAL ARTICLE)  
LA English  
FS Priority Journals; Cancer Journals  
EM 9202  
L9 ANSWER 4 OF 9 MEDLINE  
DUPLICATE 3

L9 ANSWER 1 OF 9 MEDLINE  
AN 92201186 MEDLINE  
TI The primary structure and gene organization of human substance P and neuropeptide Y receptors.  
AU Takahashi K; Tanaka A; Hara M; Nakanishi S  
CS Institute for Immunology, Kyoto University Faculty of Medicine, Japan.  
SO EUROPEAN JOURNAL OF BIOCHEMISTRY, (1992 Mar 15) 204 (3) 1025-33.  
CY GERMANY; Germany, Federal Republic of  
DT Journal; Article; (JOURNAL ARTICLE)  
LA English  
FS Priority Journals; Cancer Journals  
OS GENBANK-X65172; GENBANK-X65173; GENBANK-X65174; GENBANK-X65175; GENBANK-X65176; GENBANK-X65177; GENBANK-X65178; GENBANK-X65179; GENBANK-X65180; GENBANK-X65181  
EM 9207  
L9 ANSWER 2 OF 9 MEDLINE  
AN 91093253 MEDLINE  
TI The human neurokinin A (substance K) receptor. Molecular cloning of the gene, chromosome localization, and isolation of the cDNA from tracheal and gastric tissues.  
AU Gerard N P; Eddy R L Jr; Shows T B; Gerard C  
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1991 Jan 15) 266 (2) 1354.  
CY United States  
DT Errata; (PUBLISHED ERRATUM)  
LA English  
FS Priority Journals; Cancer Journals  
EM 9104  
L9 ANSWER 3 OF 9 MEDLINE  
AN 92060628 MEDLINE  
TI Cloning, expression of the human substance K receptor, and analysis of its role in mitogenesis.  
AU Cyr C; South V; Saltzman A; Felder S; Ricca G A; Jaye M; Huebner K; Kagan J; Croce C M; Schlessinger J; et al  
CS Department of Pharmacology, New York University School of Medicine, New York 10016.  
SO ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, (1991) 632 426-7.  
CY United States  
DT Journal; Article; (JOURNAL ARTICLE)  
LA English  
FS Priority Journals; Cancer Journals  
EM 9202  
L9 ANSWER 4 OF 9 MEDLINE  
DUPLICATE 3



AN 91175483 MEDLINE  
 TI Cloning and expression of the human substance  
 K receptor and analysis of its role in mitogenesis  
 [published erratum appears in Cell growth Differ 1991 May;2(5):266].  
 AU Kirs R M; South V; Saltzman A; Felder S; Ricca G A; Jaye M; Huebner  
 K; Kagan J; Croce C M; Schlessinger J  
 CS Department of Pharmacology, New York University School of Medicine,  
 New York 10016.  
 NC CA25875 (NCI)  
 CA39860 (NCI)  
 SO CELL GROWTH AND DIFFERENTIATION, (1991 Jan) 2 (1) 15-22.  
 CY Journal code: AYH. ISSN: 1044-9523.  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 EM 9107  
 L9 ANSWER 5 OF 9 CAPLUS COPYRIGHT 1997 ACS  
 AN 1992:122266 CAPLUS  
 DN 116:122266  
 TI Isolation and characterization of the human lung NK-2 receptor gene  
 using rapid amplification of cDNA ends  
 AU Graham, Alexander; Hopkins, Brian; Powell, Steven J.; Danks, Petra;  
 Briggs, Ian  
 CS Biotechnol. Dep., ICI Pharm., Macclesfield/Cheshire, SK10 4TG, UK  
 SO Biochem. Biophys. Res. Commun. (1991), 177(1), 8-16  
 CODEN: BBRC99; ISSN: 0006-291X  
 DT Journal  
 LA English  
 L9 ANSWER 6 OF 9 MEDLINE  
 AN 91056095 MEDLINE  
 TI The human neurokinin A (substance K)  
 receptor. Molecular cloning of the gene, chromosome  
 localization, and isolation of cDNA from tracheal and gastric  
 tissues [published erratum appears in J Biol Chem 1991 Jan  
 15;266(2):1354].  
 AU Gerard N P; Eddy R L Jr; Shows T B; Gerard C  
 CS Department of Medicine, Beth Israel Hospital, Boston,  
 Massachusetts.  
 NC HL41587 (NHLBI)  
 HL01777 (NHLBI)  
 SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1990 Nov 25) 265 (33) 20455-62.  
 CY United States  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals; Cancer Journals  
 OS GENBANK-J05680; GENBANK-M57414; GENBANK-M57415; GENBANK-M60281;  
 GENBANK-M60282; GENBANK-M60283; GENBANK-M60284  
 EM 9103  
 L9 ANSWER 7 OF 9 BIOSIS COPYRIGHT 1997 BIOSIS  
 AN 91:84935 BIOSIS  
 DN BR40:38920  
 TI CLONING EXPRESSION AND BIOCHEMICAL ANALYSIS OF HUMAN  
 SUBSTANCE K RECEPTOR IN NIH 3T3 CELLS.





AU KRIS R M; CYR C  
 CS DEP. PHARMACOL., 550 FIRST AVE., N.Y.U. MED. CENT., NEW YORK, N.Y.  
 10016.  
 SO 20TH ANNUAL MEETING OF THE SOCIETY FOR NEUROSCIENCE, ST. LOUIS,  
 MISSOURI, USA, OCTOBER 28-NOVEMBER 2, 1990. SOC NEUROSCI ABSTR 16  
 (1). 1990. 7. CODEN: ASNEE5  
 DT Conference  
 LA English  
 L9 ANSWER 8 OF 9 CAPLUS COPYRIGHT 1997 ACS  
 AN 1990:1725 CAPLUS  
 DN 112:1725  
 TI A conserved gene 3' to the HPFH-1 deletion breakpoint may have an  
 effect on fetal globin gene expression in HPFH-1  
 AU Penny, Laura A.; Forget, Bernard G.  
 CS Sch. Med., Yale Univ., New Haven, CT, 06510-8056, USA  
 SO Prog. Clin. Biol. Res. (1989), 316B(Hemoglobin Switching, Pt. B),  
 133-41  
 CODEN: PCBRD2; ISSN: 0361-7742  
 DT Journal  
 LA English  
 L9 ANSWER 9 OF 9 MEDLINE  
 AN 89240203 MEDLINE  
 TI Substance P and substance K receptor  
 binding sites in the human gastrointestinal tract:  
 localization by autoradiography.  
 AU Gates T S; Zimmerman R P; Mantyh C R; Vigna S R; Maggio J E; Welton  
 M I; Passaro E P Jr; Mantyh P W  
 CS Center for Ulcer Research and Education, VA Medical  
 Center-Wadsworth, Los Angeles, CA 90073.  
 NC NS 23970 (NINDS)  
 SO PEPTIDES, (1988 Nov-Dec) 9 (6) 1207-19.  
 Journal code: PA7. ISSN: 0196-9781.  
 CY United States  
 DT Journal; Article; (JOURNAL ARTICLE)  
 LA English  
 FS Priority Journals  
 EM 8908

DUPLICATE 5

